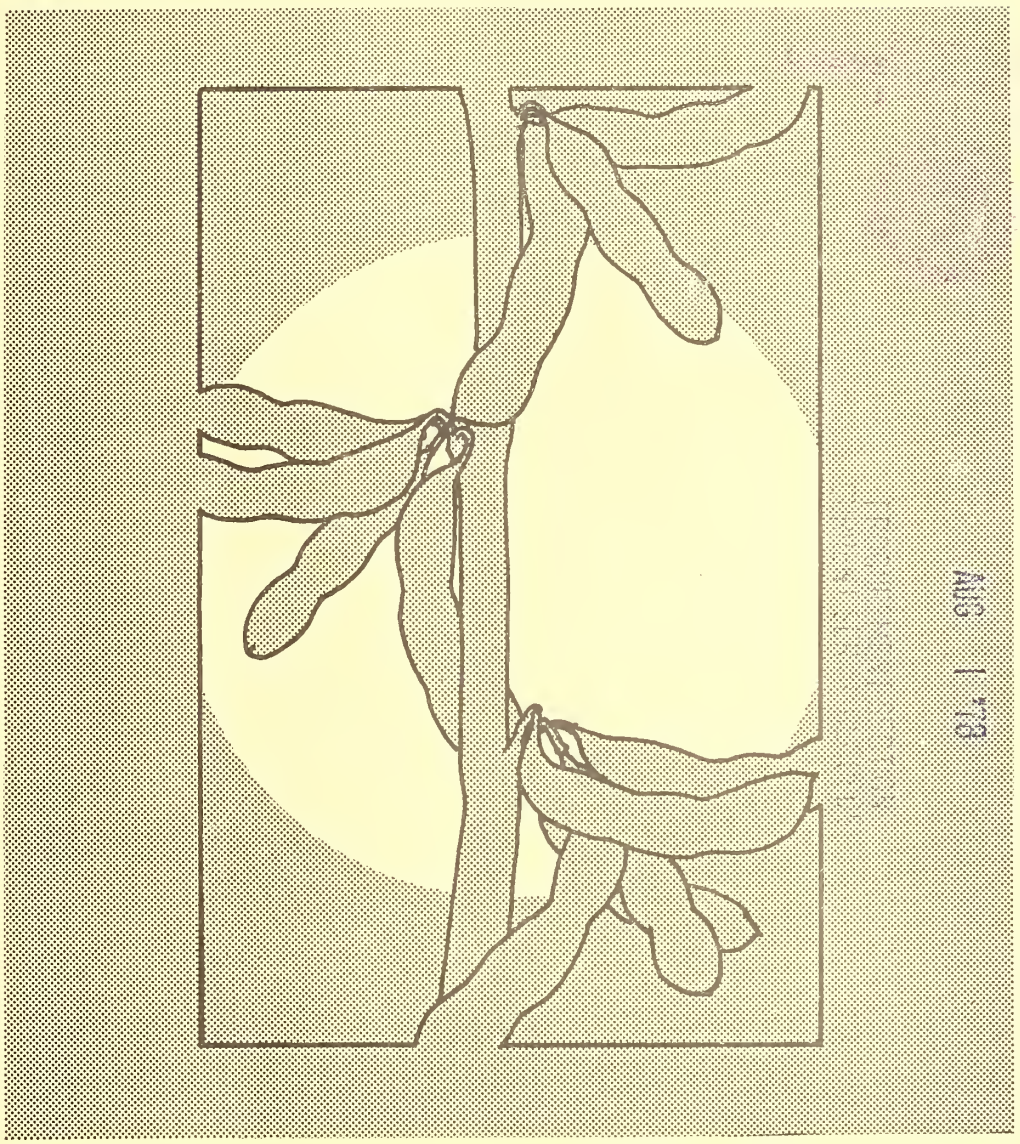
Soybean Genetics Newsletter



Volume 5 April 1978

Agricultural Research Service - USDA
Department of Agronomy
and Department of Genetics
Iowa State University
Ames, Iowa 50011

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I. FOREWORD

As the tempo of soybean research increases all over the world, the Soybean Genetics Newsletter has engendered a corresponding increase in interest, participation and scope. The diversity and range of the articles contributed, from all over the world, reflect the importance of protein crops in general and soybeans in particular to crop breeders, geneticists and agronomists.

Volume 5 of the Newsletter shows a steadily growing mailing list, from more than 50 countries, and contains a greatly expanded list of publications of interest to soybean scientists. This expanded list indicates a proliferation of literature in the field. The production crew of Volume 5 consisted of technicians Pat Muir and Holly Heer, and graduate students Steve Broich, Barbara Smith, Dave Stelly and Carol Winger.

The United States Department of Agriculture continues to support the Soybean Genetics Newsletter, making it possible to mail it to interested scientists, upon request, without charge.

--Reid G. Palmer

II. ANNOUNCEMENTS

Plant Breeding Symposium II, sponsored by Iowa State University at the new Iowa State Center, will be held March 12-16, 1979. The symposium will review plant breeding advances of the past 15 years, and evaluate areas of future potential.

Ten half-day sessions will consider the following topics:

1) Progress in Meeting Human Needs through Plant Breeding
2) Exotic Germplasm; Resources and Utilization
3) Application of Tissue Culture to Plant Improvement
4) Morphological and Physiological Traits
5) Selection and Breeding Methods
6) Chromosomal and Cytoplasmic Manipulations
7) Breeding for Stress Environments
8) Pest Resistance
   - Pathology
   - Entomology
9) Development of Plants for Multiple-Cropping Systems
10) Improvement of Nutritional Quality

For registration information please contact:

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PLANT BREEDING SYMPOSIUM II

MARCH 12 - 16, 1979

sponsored by IOWA STATE UNIVERSITY

For Information Contact:

Dr. K.J. Frey, chairman
Agronomy Department
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Ames, Iowa 50011

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ANNOUNCEMENT

The first volume of the Soybean Rust Newsletter has been published by the International Working Group on Soybean Rust on December, 1977. Single copies of the newsletter can be obtained free by writing to:

Mr. S. Shanmugasundaram
Secretary, IWGSR
AVRDC, P.O. Box 42
Shanhua, Tainan 741, Taiwan
R.O.C.

REQUEST FOR CONTRIBUTIONS TO THE SECOND ISSUE OF "SOYBEAN RUST NEWSLETTER"

Research articles, reports, notes, announcement of resistant or tolerant germplasm, and any other news item related to soybean rust are requested, and they will be accepted until August 31, 1978. Address all correspondence regarding the SRN to the above address.

RULES FOR CONTRIBUTORS

1) Information in the SRN will be informal to stimulate the exchange of ideas and information among soybean rust scientists. SRN articles may be preliminary in nature and speculative in content, and should not be regarded as equivalent to papers published in formal scientific journals. Even so, such reports can be very valuable and helpful, if viewed in the proper perspective. Data presented in the SRN are not to be used in other publications without the consent of the respective authors.

2) Contributions should be in English, typed double spaced and not more than four 8½" by 11" pages. You may send as many separate contributions as you wish. Send two copies for each article.

3) Correspondence regarding an article should be on a separate page.

4) Photographs should be glossy black/white prints of high quality with good dark and light contrasts. Drawings for graphs and charts should be prepared with India ink on good quality tracing paper. Typewritten matter is not usually acceptable on graphs and charts. A good size for photographs is 5" by 7" and drawings is what will fit on an 8½" by 11" page.

5) Except for possible minor editing, manuscripts will be published as received from contributors.

6) Title your report, place your name(s), name of university, institution or company under the title. Please give complete address. (For contributors outside Taiwan (R.O.C.): please send reports by airmail.)

7) Citations of recent publications are most welcome.

ANNOUNCEMENT

NATIONAL TECHNICAL EDITOR CLEARANCE NOT REQUIRED FOR NEWSLETTER ARTICLES

Some USDA employees have expressed concern about getting NTE clearance for newsletter items such as for the Soybean, Barley, Corn, Wheat and Oat Newsletters. AM 152, "Manuscript Clearance for non-USDA Media" does not speak specifically to newsletters, and SEA policy does not require peer review nor NTE clearance of such contributions. Newsletters are considered informal communications among workers in well-defined research areas. They may not be cited nor do they constitute publications in terms of research evaluations.

ANNOUNCEMENT

The Agricultural Research Service of the U.S. Department of Agriculture announces the publication of Proceedings of the Workshop on Soybean Rust in the Western Hemisphere.

Edited by Nader G. Vakili, the Proceedings is a complete report on the meetings held November 14-17, 1976, at the Mayaguez Institute of Tropical Agriculture in Mayaguez, Puerto Rico.

During the summer of 1976, several soybean varieties and edible bean species growing in experimental plots at 500 meters elevation at the Adjuntas Agricultural Experiment Station, Limani, Puerto Rico, were found to be naturally infected with a Phakopsora rust. Mycological examinations identified the organism as Phakopsora pachyrhizi Sydow.

Strains of this organism found in the Eastern Hemisphere have had a serious depressing effect on production of soybeans when not controlled. Its appearance in Puerto Rico was cause for real concern about its virulence and potential for spread to soybean cultivars grown in the major production areas of the United States.

An early step in responding to this threat was the convening of a workshop, to bring together scientists, plant disease regulation personnel, program administrators and other interested persons to review and discuss the problem and how to cope with it. This volume contains a record of the discussions and recommendations.

With a January 1978 publication date, this 82-page publication is available, while supplies last, single copies free, from the Mayaguez Institute of Tropical Agriculture, P.O. Box 70, Mayaguez, Puerto Rico, 00708.

III. REPORT OF SOYBEAN GENETICS COMMITTEE

A) The current members of this committee and the expiration dates of their terms are:

H. R. Boerma (1980)
Dept. of Agronomy
University of Georgia
Athens, GA 30602

R. I. Buzzell (1979)
Agr. Canada, Res. Station
Harrow, Ontario, NOR 1GO
Canada

H. H. Hadley, Chm. (1979)
Dept. of Agronomy
University of Illinois
Urbana, IL 61801

T. Hymowitz (1981)
Dept. of Agronomy
University of Illinois
Urbana, IL 61801

T. C. Kilen, USDA (1980)
Delta Branch Exp. Station
Soybean Prod. Res.
Stoneville, MS 38776

R. G. Palmer, USDA
(Editor of Soybean Genetics Newsletter)
Dept. of Genetics
Iowa State University
Ames, IA 50011

J. R. Wilcox, USDA (1981)
Dept. of Agronomy
Purdue University
West Lafayette, IN 47907

B) Organization of the Committee:

1) The Committee will be composed of six elected members and the editor of the Soybean Genetics Newsletter.

2) The term of the elected members will be three years. After a member has been off for one year, he (she) can be reelected. The Committee will elect two new members each year; a simple majority is needed for election. The members will be elected prior to February 1 of each year, by a mail ballot conducted by the chairman.

3) At the annual meeting of the Committee (usually in February in conjunction with the Soybean Breeding and Genetics Workshop), the two new members and the two retiring members of the Committee are eligible to attend and vote.

4) The Chairman will be elected at the annual Committee meeting and serve through the next annual meeting, and may be reelected.

C) The duties of this Committee were reviewed and revised at Memphis, TN, February 20, 1978, and the following procedures were approved:

1) Maintain Genetic Collection.

The Genetic Collection is divided into four categories:

a) Type Collection includes all published genes of soybeans, preferably in the original strains (excluding U.S. and Canadian name varieties, which are maintained in a separate collection) plus certain mutants or strains that appear to the Committee to have potential genetic interest.

b) Isoline Collection includes adapted varieties Clark, Harosoy and Lee, into which have been backcrossed single genes or combinations of genes. Also included are certain genes or combinations with Chippewa, Wayne and Williams.

c) Linkage Collection includes linkage combinations and the various genetic recombinations.

d) Cytological Collection includes translocations, inversions, deficiencies, trisomics, tetraploids, etc.

Collections a, b and c are maintained at Urbana, Illinois, with R. L. Bernard as curator. Collection d is maintained at Ames, Iowa, with R. G. Palmer as curator.

D) Manuscript review and genetic symbol approval.

The Soybean Genetics Committee requests that researchers submit all manuscripts concerning qualitative genetic interpretation and symbols to the Committee Chairman. This review by the Genetics Committee will serve to insure orderly identification and use of genetic nomenclature and to avoid conflict of symbols. This will also allow assignment of type collection designations (T-numbers) prior to publication, so that these T-numbers may be used in the journal article to identify parental lines.

E) Soybean Genetics Newsletter notes.

All notes for the Newsletter should be sent to the SGN editor, R. G. Palmer, who will ask the Soybean Genetics Committee to review those articles concerning qualitative genetic interpretation and symbols. Genetic symbols reported in the Newsletter will have the same status as those published in scientific journals.

Rules for Genetic Symbols

I) Gene Symbols

a) A gene symbol shall consist of a base of one to three letters, to which may be appended subscripts and/or superscripts as described below.

b) Genes that are allelic shall be symbolized with the same base letter(s) so that each gene locus will be designated by a characteristic symbol base.

c) The first pair of genes reported for a gene locus shall be differentiated by capitalizing the first letter of the symbol for the dominant or partially dominant allele. (Example: Ab, ab. Ab is allelic and dominant to ab.) If genes are equivalent, codominant, or if dominance is not consistent, the capitalized symbol may be assigned at the author's discretion.

d) When more than two alleles exist for a locus, the additional alleles or those symbolized subsequently to the pair first published shall be differentiated by adding one or two uncapitalized letters as a superscript to the base. (Example: R, r^{m}, r.) This shall be the only use of superscripts. The base for the additional alleles is capitalized only when the gene is dominant or equivalent to the allele originally designated with a capitalized symbol. The superscript may be an abbreviation of a descriptive term. When allelism is discovered for a gene previously assigned a symbol, the previous symbol may be used as the superscript.

e) Gene pairs with the same or similar effects (including duplicate, complementary, or polymeric genes) should be designated with the same letter base differentiated by numerical subscripts, assigning 1, 2, 3, 4, etc., consecutively in the order of publication. (Example: The y series for chlorophyll deficiency.) This shall be the only use of subscripts. Letter subscripts should not be used. The subscript 1 is automatically a part of the first reported gene symbol for each base but may be omitted until the second symbol is assigned.

f) Base letters may be chosen so as to indicate apparent relationships among traits by using common initial letters for all loci in a related

group of traits. Examples are P for pubescence type, R for disease reaction (plus two initials of the pathogen to complete the base), and L for leaf shape.

g) The distinction between traits that are to be symbolized with identical, similar, or with unrelated base letters is necessarily not clear cut. The decision for intermediate cases is at the discretion of the author but should be in accordance with previous practices for the particular type of trait. The following sections concern supplementary symbols that may be used whenever desired as aids to presentation of genetic formulas.

h) A dash may be used in place of a gene symbol to represent any allele at the indicated locus. The locus represented should be apparent from its position in the formula. (Example: A_ represents both AA and Aa.)

i) A question mark may be used in place of a symbol when the gene is unknown or doubtful, or it may be used as a superscript to the base symbol for the same purpose. (Example: $a^{?}$ indicates that the latter is an unknown allele at the A locus.)

j) Plus symbols may be used in place of the assigned gene symbols of a designated standard homozygous strain when this will facilitate presenting genetic formulas. The standard strain may be any strain selected by the worker, as long as the strain being used and its genetic formula are made explicit.

II) Linkage and Chromosome Symbols

a) Linkage groups and the corresponding chromosomes shall be designated with Arabic numerals. Linkage shall be indicated in a genetic formula by preceding the linked genes with the linkage group number and listing the gene symbols in the order that they occur on the chromosome.

b) Permanent symbols for chromosomal aberrations shall include a symbol denoting the type of aberration plus the chromosome number(s) involved. Specific aberrations involving the same chromosome(s) shall be differentiated by a letter as follows: The symbol Tran shall denote translocations. Tran 1-2a would represent the first case of reciprocal translocations between chromosomes 1 and 2, Tran 1-2b the second, etc.

The symbol Def shall denote deficiencies, Inv inversions, and Tri primary trisomics. The first published deficiency in chromosome 1 shall be symbolized as Def 1a, the second as Def 1b, etc. The first published inversion in chromosome 1 shall be denoted as Inv 1a, etc. The first published primary trisomic shall be designated with the Arabic numeral that corresponds to its respective linkage group number.

c) Temporary symbols for chromosomal aberrations are necessary, as it may be many years before they are located on their respective chromosomes. Tran 1 would represent the first case of a published reciprocal translocation; Tran 2, the second case, etc. The first published deficiency shall be symbolized as Def A, the second as Def B, etc. The first published inversion shall be symbolized as Inv A, the second as Inv B, etc. The first published primary trisomic shall be designated as Tri A, the second as Tri B, etc. When appropriate genetic and/or cytological evidence is available, the temporary symbols should be replaced with permanent symbols, with the approval of the Soybean Genetics Committee.

III) Cytoplasmic Factor Symbols

a) Cytoplasmic factors shall be designated with one or more letters prefixed by cyt-. (Example: cyt-G indicates the cytoplasmic factor for maternal green cotyledons, cyt-Y indicates that for maternal yellow cotyledons.)

IV) Priority and Validity of Symbols

a) A symbol shall be considered valid only when published in a recognized scientific journal, or when reported in the Soybean Genetics Newsletter, with conclusions adequately supported by data which establish the existence of the entity being symbolized. Publication should include an adequate description of the phenotype in biological terminology, including quantitative measurements wherever pertinent.

b) In cases where different symbols have been assigned to the same factor, the symbol first published should be the accepted symbol, unless the original interpretation is shown to be incorrect, the symbol is not in accordance with these rules, or additional evidence shows that a change is necessary.

V) Rule Changes

a) These rules may be revised or amended by a majority vote of the Soybean Genetics Committee.

IV. NEW GENE SYMBOLS APPROVED BY SOYBEAN GENETICS COMMITTEE

New gene symbols approved at the 1978 meeting of the Soybean Genetics Committee at their meeting in Memphis, TN, February 20 include:

$\underline{y}^{19}$	for delayed "albino"
rmd	for resistance to powdery mildew
$\underline{sb}_1$ and $\underline{sb}_2$	for brachytic dwarf
$\underline{t}_1$	for absence of Kunitz trypsin inhibitor
le	for absence of lectin, a protein with high molecular weight
$\underline{rym}_1$ and $\underline{rym}_2$	for resistance to yellow mosaic

V. RESEARCH NOTES

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1) Soybean linkage tests.

F_2 linkage results are presented in Table 1 with a = XY, b = Xy, c = xY, and d = xy for the gene pairs listed in the form of Xx and Yy. Percentage recombination was obtained from the ratio of products following Immer and Henderson (1943).

There is a single dominant gene which results in delayed flowering ("late") vs. non-delayed ("early") flowering for the recessive allele, under a 20-hr daylength using incandescent light (unpublished results and Buzzell et al., 1974). The recessive gene was obtained from PI 297.550 (Polson, 1972). Results from testing F_2 plants for flavonol class and testing F_3 progenies for daylength response indicate that this locus is not linked to $\underline{Fg}_1/\underline{fg}_1$ in Linkage Group 5.

Results from rating the F_2 for pubescence color and from progeny testing for adult plant resistance to powdery mildew (Buzzell and Haas, 1978) indicate that Rmd/rmd might be in Linkage Group 1.

Table 1
Soybean F_2 linkage tests

Genes	a	b	c	d	Sum	%R	SE	Phase
OX633 ($\underline{fg}_1$ early $\underline{e}_3$) x OX318 ($\underline{Fg}_1$ late $\underline{e}_3$)								
$\underline{Fg}_1$ $\underline{fg}_1$ Late Early	41	16	19	5	81	I	-	c
Harosoy 63 (t rmd) x Altona (T Rmd)								
T t Rmd rmd	68	16	17	6	107	44.4	6.8	c

References

Buzzell, R. I., B. R. Buttery and J. H. Haas. 1974. Soybean genetic studies at Harrow. Soybean Genet. Newsl. 1: 9-11.

Buzzell, R. I. and J. H. Haas. 1978. Inheritance of adult plant resistance to powdery mildew in soybeans. Can. J. Genet. Cytol. 20: (In press).

Immer, F. R. and M. T. Henderson. 1943. Linkage studies in barley. Genetics 28: 419-440.

Polson, D. E. 1972. Day-neutrality in soybeans. Crop Sci. 12: 773-776.

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1) A possible alternate explanation for light green spots on yellow leaves in the soybean $\underline{y}_{11}\underline{y}_{11}$ test system.

Soybean has a gene $\underline{Y}_{11}$ which is involved in chlorophyll synthesis and is incompletely dominant. This means that the homozygous recessive ($\underline{y}_{11}\underline{y}_{11}$) is yellow and seedling lethal, the homozygous dominant ($\underline{Y}_{11}\underline{Y}_{11}$) is dark green, and the heterozygote ($\underline{Y}_{11}\underline{y}_{11}$) is medium green (a yellowish green) and viable. Because a crossover in the heterozygote would produce a dark green/yellow twin spot on a medium green background, the system has been extensively exploited by Vig and Paddock (1968 and 1969) and Vig (1971, 1972, 1973 and 1975) as a tester system for chemicals suspected of mutagenic activity. As a further refinement of the test system, Vig has suggested that light green spots on yellow leaves can only arise from a back mutation of $\underline{y}_{11}$ to $\underline{Y}_{11}$, and that such spots therefore offer a means of detecting point mutations (Vig, 1973 and 1975).

While this is a logical explanation, the occurrence of a large number of these light green spots on yellow leaves of seedlings which had been treated as seeds with .01% mitomycin C (a drug known for its ability to produce somatic crossing over via chromosome breakage and reunion [Cohen and Shaw, 1964; Huttner and Ruddle, 1976; and Holliday, 1964], but not reputed to produce point mutations) was difficult to understand.

An explanation for this apparent discrepancy between the above observation and the known activity of the drug may reside in the work of Sears (1953). He found that in some cases in wheat the loss of a locus on one chromosome

through monosomy resulted in the homologous recessive allele expressing a dominant phenotype. Sears called this class of genes "hemizygous ineffective recessives" and postulated that the effect might be related to the polyploid nature of wheat.

Since soybeans may also be polyploid and therefore possibly subject to the same phenomenon, it seems appropriate to call it to the attention of those who may be planning to use the $\underline{Y}_{11}\underline{y}_{11}$ test system. Situations which might be expected to give rise to a hemizygous ineffective recessive expressing a dominant phenotype would include deletions or monosomy arising through nondisjunction. Therefore, while light green spots on yellow leaves may indeed result in some (or perhaps in all) cases from point mutations, it is suggested that the alternate interpretation of $\underline{y}_{11}$ as a hemizygous ineffective recessive gene should also be taken into consideration.

References

Cohen, M. M. and M. W. Shaw. 1964. Effect of mitomycin C on human chromosomes. J. Cell Biol. 23: 386-395.

Holliday, R. 1964. The induction of mitotic recombination by mitomycin C in Ustilago and Saccharomyces. Genetics 50: 323-335.

Huttner, K. M. and F. H. Ruddle. 1976. Study of mitomycin C induced chromosomal exchange. Chromosoma 56: 1-13.

Sears, E. R. 1953. Nullisomic analysis in common wheat. Am. Nat. 87: 245-252.

Vig, B. K. 1971. Increases induced by colchicine in the incidence of somatic crossing over in Glycine max. Theoret. Appl. Genet. 41: 145-149.

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Vig, B. K. 1973. Somatic crossing over in Glycine max (L.) Merrill: Mutagenicity of sodium azide and lack of synergistic effect with caffeine and mitomycin C. Genetics 75: 265-277.

Vig, B. K. 1975. Soybean Glycine max: A new test system for study of genetic parameters as affected by environmental mutagens. Mutat. Res. 31: 49-56.

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Vig, B. K. and E. F. Paddock. 1970. Studies on the expression of somatic crossing over in Glycine max L. Theoret. Appl. Genet. 40: 316-321.

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1) Sterility mutants in soybeans.

In 1975 we selected green, partially sterile plants in farmers' fields when the normal plants had dropped their leaves and were ready for harvest. Seeds were harvested from the off-type plants and planted in the greenhouse (1975-76). The resulting plants which we called "F_1's" were normal. Their progenies ("F_2's") were grown in 1976 in the field and "F_3's" were grown in 1977. Because of lack of greenhouse space, 'Calland' was not grown until a year later and so is one generation behind 'Wayne' and 'Woodworth'.

Segregation in F_2 and F_3 generations indicates that all three mutants are male steriles caused by single recessive genes (Table 1), i.e., Ms __ is male fertile and ms ms is male sterile. In Wayne, 38 F_3 rows segregated and 14 bred true, which fits a 2:1 ratio ($\chi^2 = 0.96$, $P = .33$). In Woodworth, the observed ratio was 50 to 24 which also fits a 2:1 ratio quite well ($\chi^2 = .03$, $P = .86$). All three male steriles have empty anthers but otherwise apparently normal flowers. Distributions of one-, two-, three- and four-seeded pods on male sterile segregates indicate rather high female fertility (Table 2). Mean number of seeds per pod was approximately two, with Woodworth being somewhat higher than Wayne. This cultivar may have a natural tendency for more four-seeded pods than Wayne has. It is interesting that two-seeded pods are lower in frequency than both three-seeded and one-seeded pods (with one exception). We have no explanation to offer at this time.

We do not yet know what loci are involved. Crosses of the type ms_1ms_1 x Ms_xms_x were made in the field this summer between Wayne, Woodworth, 'Northrup-King', 'Rampage', and ms_2ms_2 stocks. Northrup-King and Rampage stocks were obtained from R. G. Palmer and ms_2ms_2 from R. L. Bernard. One F_1 from ms ms Rampage x Ms ms Woodworth and one F_1 from ms ms Northrup-King x Ms ms Wayne were male sterile. Thus we probably have not discovered a new ms locus. Our observations, however, suggest that if one desires a male sterile form in a particular variety he might seriously consider searching for a mutant rather than use a backcross program with known male steriles. Large populations can be screened effectively at harvest time. Male steriles can probably be separated from other sterile types by the presence of a high frequency of two-, three-, or even four-seeded pods. Sterile types with mostly one-seeded pods

Table 1

Distribution of male fertile and male sterile segregates in "F_2" and "F_3" generations in three soybean cultivars

Cultivar	Generation	Male fertile	Male sterile	n	χ^2(3:1)	P
Calland	F_2	97	37	134	0.49	0.48
Wayne	F_2	35	15	50	0.67	0.41
	F_3	356	140	496†	2.75	0.10
Woodworth	F_2	66	26	92	2.09	0.15
	F_3	459	162	621†	0.39	0.53

†From 20 segregating progenies. Progenies were homogeneous, χ^2's being 18.34 (P = .50) and 18.47 (P = .49) for Wayne and Woodworth respectively.

Table 2

Number of seeds per pod on male sterile segregates in Wayne and Woodworth soybeans

Cultivar	Generation	Number of seeds per pod				Pod no.	$\bar{X}$/pod
		1	2	3	4		
Wayne	F_2	36	41	43	--	120	1.94
Woodworth	F_2	133	109	158	7	407	2.10
Wayne	F_3	120	92	115	1	328	1.99
Woodworth	F_3	101	90	129	16	336	2.18

are probably female sterile also.

In 1976, we crossed noduleless 'Clark' by a partial sterile (received several years ago from C. R. Weber at Ames, Iowa). This type tends to have multiple pistils but expressivity varies so that 1 to 5 pistils occur in different flowers on the same plant. Attempts to cross the multipistillate line as female were unsuccessful. One cross was obtained from the line used as a male. A small F_2 population of 63 plants was observed in the field in 1977,

giving 56 fertile to 7 partially sterile. Too few partial steriles occurred to fit a 3:1 ratio. This may have resulted from some genetically partial steriles having such a low percentage of multipistillate flowers that they were classified as normal. Flower color and nodulation behavior also segregate or should segregate in the same material. Nodulation data has not yet been obtained. Flower color showed no association with sterility: fertile, purple—42; fertile, white—14; partially sterile, purple—6; partially sterile, white—1. An F_3 progeny test will be conducted in 1978.

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S. J. Openshaw
J. C. Pennell

2) Screening the USDA soybean germplasm collection for Kunitz trypsin inhibitor variants.*

The trypsin inhibitors as a group form one of the major anti-nutritional factors in soybean [Glycine max (L.) Merrill] seed. Several different trypsin inhibitors have been reported to be present in soybeans. However, much of the soybean trypsin inhibitor activity is thought to be due to the protein SBTI-A_2 which is generally known as the Kunitz trypsin inhibitor.

Seed from the USDA soybean germplasm collection have been screened using polyacrylamide gel electrophoresis for the presence or absence of electrophoretic forms of SBTI-A_2. Thus far, four electrophoretic forms have been discovered (Hymowitz and Hadley, 1972; Orf and Hymowitz, 1977a; Orf et al., 1977; and Singh et al., 1969). Three of the forms designated Ti^1, Ti^2 and Ti^3 are electrophoretically distinguishable from one another by their different Rf values of 0.79, 0.75 and 0.83, respectively (Rf = mobility relative to the dye front in a 10% polyacrylamide gel anodic system using a pH 8.3 Tris-glycine

*We wish to acknowledge the assistance of R. L. Bernard and E. E. Hartwig who provided us with the seed. Research supported in part by the Illinois Agricultural Experiment Station and a grant from the Illinois Crop Improvement Association. Dr. N. Kaizuma was supported by a grant provided by the Ministry of Education, Japan. Permanent address of Dr. Kaizuma is the Faculty of Agriculture, Iwate University, Morioka, Iwate, Japan. Dr. H. Skorupska was supported in part by the Eastern European Agricultural Exchange Program conducted by the Church of the Brethren. Permanent address of Dr. Skorupska is the Institute of Genetics and Plant Breeding, Academy of Agriculture, Poznan, Poland.

buffer). The three forms are controlled by a codominant multiple allelic system at a single locus. The fourth form does not exhibit a SBTI-A_2 protein band in the gels. The lack of a protein band is inherited as a recessive allele. The gene for the lack of the SBTI-A_2 protein band has been designated ti.

The summary of the screening data is presented in Table 1. Of the 3038 soybean accessions tested, 2698 accessions, or 88.8%, had the Ti^1 allele. The Ti^2, Ti^3 and ti alleles were found in 10.9, 0.3 and 0.06% of the population studied. Of the 359 accessions of Glycine soja tested, 337 accessions had Ti^1 and 24 accessions had Ti^2. Two accessions of Glycine soja, PI 378.694 and PI 407.258, were mixtures containing both Ti^1 and Ti^2 seed.

Sources for the Ti^2 allele within the Named Variety Collection are 'Aoda', 'Goku', 'Hakote', 'Jefferson', 'Jogun', 'Jogun (Ames)', 'Miller 67',

Table 1

Distribution of Kunitz trypsin inhibitor variants in the USDA soybean germplasm collection*

Collection		Ti^1	Ti^2	Ti^3	ti	Total
Asia:	Japan	284	187	6		477
	Korea	366	48	1	2	417
	China	794	9			803
	Remainder	345	37	1		383
Europe		405	29			434
Africa		56				56
Other:	Named Varieties	320	15			335
	Type Collection	89	5			94
	'G. gracilis'	39				39
	G. soja†	337	24			361

*Data taken in part from Clark et al., 1970; Hymowitz et al., 1971; Kaizuma and Hymowitz, 1978; Orf, 1976; and Skorupska and Hymowitz, 1978.

†Two accessions PI 378.694 and PI 407.258 were mixtures containing both Ti^1 and Ti^2 seed.

'Polysoy', 'Rokusun', 'Sato-3', 'Sousei', 'Toku', 'Tokyo', 'Tortoise Egg' and 'Wolverine'. Sources for the $\underline{Ti}^2$ allele within the Type Collection are T69, T136, T141, T216 and T245.

Sources for the $\underline{Ti}^3$ allele are PI 86.084, PI 196.172, PI 205.384, PI 227.557, PI 246.367, PI 304.217, PI 342.002 and PI 360.844. Sources for the ti allele are PI 157.440 and PI 196.168.

The screening and inheritance study phases of the project essentially are completed. However, the feeding trial phase of the project will increase in importance (Bajjalieh et al., 1977; Yen et al., 1971, 1973 and 1974). At present, feeding trials have been initiated to compare the nutritive value of raw defatted soybean meal from an accession without the Kunitz trypsin inhibitor with accessions containing the Kunitz trypsin inhibitor. In addition, linkage tests are being carried out to determine whether the Kunitz trypsin inhibitor is linked to certain chemical components of seed or certain morphological characters of plants (Orf and Hymowitz, 1977b).

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3) Soybean linkage tests between two seed proteins and other characters.*

F_2 linkage results between *Ti* and W_1, Dt_1 and *Ep* are shown in Table 1. F_2 linkage results between Sp_1 and W_1, Dt_1, *Ep* and *Le* are shown in Table 2. In all cases the Chi-square values were calculated using contingency tables. Since all the probabilities are greater than .05, none of the gene pairs considered appear to be linked. Previously we have reported on the independent inheritance between *Ti* and Sp_1 (Orf and Hymowitz, 1977).

The *Ti* and Sp_1 F_2 genotypes were determined using previously described procedures (Hymowitz and Hadley, 1972; Orf and Hymowitz, 1976). The *Ep* phenotype was determined using the test described by Buttery and Buzzell (1968). The *Le* phenotype (*Le* controls a seed lectin; see Pull *et al.*, pages 66-70 of this issue) was determined using polyacrylamide gel electrophoresis as described by Orf *et al.* (n.d.).

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Table 1

Observed numbers of individuals in the respective phenotypic classes for F_2 linkage tests between *Ti* and W_1, Dt_1 and *Ep* from the cross 'Jefferson' (Ti^2 w_1 dt_1 *ep*) x 'Wilson' (Ti^1 W_1 Dt_1 *Ep*)

Phenotypes	Ti^1Ti^1	Ti^1Ti^2	Ti^2Ti^2	χ^2(2 df)	P
W_1 —	42	82	53	1.97	0.37
w_1 w_1	9	25	21		
Dt_1 —	34	83	50	3.11	0.21
dt_1 dt_1	17	24	24		
Ep —	40	80	55	0.31	0.86
ep ep	11	27	19		

Table 2

Observed numbers of individuals in the respective phenotypic classes for F_2 linkage tests between Sp_1 and W_1, Dt_1, *Ep* and *Le* from the crosses Jefferson (Sp_1^a w_1 dt_1 *ep*) x Wilson (Sp_1^b W_1 Dt_1 *Ep*) and 'Amsoy' (Sp_1^a *Le*) x T102 (Sp_1^b *le*)

Phenotypes	$Sp_1^aSp_1^a$	$Sp_1^aSp_1^b$	$Sp_1^bSp_1^b$	χ^2(2 df)	P
W_1 —	44	84	49	0.97	0.62
w_1 w_1	11	31	13		
Dt_1 —	42	83	42	1.06	0.59
dt_1 dt_1	13	32	20		
Ep —	40	91	44	1.77	0.41
ep ep	15	24	18		
Le —	20	49	23	1.68	0.43
le le	8	11	9		

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1) Velvetbean caterpillar resistance in soybean selections from crosses involving Mexican bean beetle resistant plants.

Segregating populations arising from crosses involving two sources of Mexican bean beetle (Epilachna varivestis Mulsant) resistance were screened and selected for resistance to velvetbean caterpillar (Anticarsia gemmatalis Hubner) in Guaiba, Rio Grande do Sul, Brazil and Isabela, Puerto Rico. The Mexican bean beetle resistant cultivars used in the crosses were PI 171.451 and PI 229.358 (Van Duyn et al., 1971). The materials tested came from two sources: Dr. R. L. Bernard of the USDA Regional Soybean Laboratory, Urbana, IL and Dr. S. G. Turnipseed of Clemson University, Blackville, SC.

The Illinois material consisted of remnant F_2 seed of seven crosses of several Midwest varieties and PI 171.451 and PI 229.358. In late 1972, these F_2 populations were planted at Guaiba in single rows bordered on one side by the variety 'Clark 63' and on the other side by the variety 'Davis'. Plants which exhibited substantially less damage than either Clark 63 or Davis were tagged during the growing season and individually harvested. A total of

66 F_2 plants were selected. Velvetbean caterpillar was the predominant foliage feeder present, and defoliation on both Clark 63 and Davis reached 70%. Progeny of the selected F_2 plants were planted at Guaiba in October, 1973. When seed supply permitted, two 2-m rows of each line were planted; otherwise, only one row was planted. Each row was bordered by Davis on both sides. The lines were visually rated for level of defoliation relative to the adjacent rows of Davis, and 150 plants were selected from 38 of the 66 F_3 lines grown.

The South Carolina material was also planted at Guaiba in October, 1973 and consisted of 251 F_5 to F_7 lines which had been previously selected for resistance to Mexican bean beetle. Most of the lines had PI 229.358 in their parentage. In total, 224 individual plants were selected from 112 of the 251 lines.

In October, 1974, the 374 lines (224 from the South Carolina material and 150 from the Illinois material) were planted at Guaiba in a randomized complete block design with two replications. Plots consisted of a single row 2.5 m long bordered on both sides by Davis. The plots were scored four times during the period of peak velvetbean caterpillar attack using the following scale:

Score	Defoliation relative to susceptible check
1	1/16
2	1/8
3	1/4
4	1/2
5	1

Defoliation reached 100% on Davis and most of the lines being evaluated. Four plants of desirable plant type were selected from each of the most resistant lines. These selections were used to continue the Brazilian program. The residual plants in each of the most resistant lines were harvested in bulk, and a portion of this seed was used to initiate the Puerto Rico evaluations.

In February, 1976, the 28 bulks from Brazil were planted at Isabela, Puerto Rico and harvested in bulk. In May, 1977, they were part of a screening of 300 cultivars and lines for resistance to defoliators at Isabela. Plots consisted of 3-m rows bordered on each side by 'Improved Pelican'. A randomized complete block design with two replications was used.

A severe infestation of velvetbean caterpillar occurred, and plots were scored on August 2 and 8, using the following scale:

Score	Defoliation relative to susceptible check
1	1/4
2	3/4
3	1

The Improved Pelican border rows as well as those of susceptible cultivars and lines in the test suffered 100% defoliation at the time of the second reading (August 8, 1977).

Defoliation scores of selected lines from Brazil and Puerto Rico are presented in Table 1. The results of these screenings indicate that the sources of resistance to Mexican bean beetle also confer some level of resistance to velvetbean caterpillar. A greater number of selected lines had PI 171.451 as a resistant parent than PI 229.358. Although many of the selections are too early for tropical environments, their improved plant type compared to the plant introductions and high level of resistance make them desirable as parents in crosses to develop tropically adapted, velvetbean caterpillar resistant cultivars.

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Table 1

Defoliation scores of soybean lines evaluated in Brazil and Puerto Rico

Line		Score*	
		Brazil	Puerto Rico
L71-4091-2/5†	Amsoy 71 x PI 171.451	3.9	2.3
L71-4091-22/5	Amsoy 71 x PI 171.451	4.1	2.5
L71-4091-24/1	Amsoy 71 x PI 171.451	4.0	3.0
L71-4091-24/3	Amsoy 71 x PI 171.451	3.5	2.5
L71-4091-30/4	Amsoy 71 x PI 171.451	4.1	1.5
L71-4093-9/1	Wayne Rpm Rps x PI 171.451	4.2	3.0
L71-4093-9/3	Wayne Rpm Rps x PI 171.451	3.5	3.0
L71-4093-9/7	Wayne Rpm Rps x PI 171.451	3.9	3.0
L71-4094-21/1	Williams x PI 171.451	4.1	3.0
L71-4094-38/2	Williams x PI 171.451	3.5	3.0
L71-4094-38/6	Williams x PI 171.451	3.8	2.8
L71-4094-41/3	Williams x PI 171.451	4.2	2.2
L71-4102-SM7/1	Cutler 71 x PI 229.358	4.2	3.0
L71-4102-38/5	Cutler 71 x PI 229.358	4.0	-
L71-4102-38/6	Cutler 71 x PI 229.358	4.1	2.8
L71-4102-38/9	Cutler 71 x PI 229.358	4.2	1.8
14/2	Bragg x PI 229.358	4.0	3.0
103/4	Bragg x PI 229.358	4.0	3.0
199/1	D66-8666 x (Bragg x PI 229.358)	4.2	2.2
611/3	York R-11 x PI 171.451	4.0	2.5
612/2	York R-11 x PI 171.451	3.8	2.2
618/1	Hardee x PI 229.358	4.1	2.8

*Amount of defoliation was scored from 1 to 5 in Brazil, where 1 = 1/16, 2 = 1/8, 3 = 1/4, 4 = 1/2, and 5 = the same as adjacent rows of Davis. In Puerto Rico, amount of defoliation was scored from 1 to 3, where 1 = 1/4, 2 = 3/4, and 3 = the same as adjacent rows of Improved Pelican.

†Lines with "L71-" designation were obtained from Illinois, the remainder were obtained from South Carolina.

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1) A new source of resistance to soybean mosaic virus.*

We have been screening tropical and temperate soybean germplasm lines to test for variation in the rate of seed transmission of soybean mosaic virus (SMV) (unpublished work of R. M. Goodman, G. R. Bowers, Jr., and E. H. Paschal II). In the course of field screening of 400 tropical soybean lines and varieties with the Illinois "severe" isolate of SMV (SMV-Il-S) we were unable to infect the cultivar 'Buffalo' (Rhod. Agric. J. 72(2): 37). Our subsequent studies have shown that Buffalo is immune to most SMV isolates and possesses a hypersensitive form of resistance to the isolates that can infect it. Here we present a preliminary report of our findings.

Buffalo was one of the 400 lines planted in July 1976 at Isabela, Puerto Rico. The planting was in hill plots, and the design was a randomized complete block replicated six times. Ten seeds were planted in each hill. At the primary leaf stage the hills were thinned to 6 plants and notes taken on the prevalence of SMV-infected seedlings arising from seeds. Then all plants in five replicates were inoculated by manually rubbing the leaves with inoculum prepared from SMV-Il-S infected soybeans (cv. 'Rampage') inoculated 14 to 21 days previously. The inoculum contained 3 ml 0.05 M sodium phosphate buffer, pH 7.0, per gram tissue (fresh weight) plus a small amount of 600 mesh carborundum and was applied with a sterilized gauze pad.

Symptom readings were taken in late July and early September, when we noted that none of the inoculated Buffalo plants were showing symptoms. We harvested the seeds of this cultivar and tested them further in the greenhouse at Urbana. There we attempted to infect several hundred seedlings over a several month period. In only one case were symptoms seen and this was also the only case in which we could demonstrate the presence of SMV infectivity in the inoculated plants. We do not know if the one plant that became infected was

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of some other variety, but this result raises the possibility of Buffalo being heterogeneous for SMV resistance. Since Buffalo was not selected for SMV resistance (indeed, its having SMV resistance was a surprise to Dr. J. R. Tattersfield, who bred this variety, personal communication), this is not an implausible possibility. Nonetheless, the vast majority of Buffalo plants inoculated at the primary leaf stage and reinoculated 2 to 3 weeks later were immune to infection by SMV-Il-S.

Subsequently, we have isolated over 100 SMV isolates from seeds obtained from the USDA soybean germplasm collections (unpublished work of E. K. Cho and R. M. Goodman). We have tentatively placed each of these isolates in one of seven groups based on their ability to infect a range of putatively SMV-resistant cultivars. Buffalo was among the cultivars used for these tests, and it was immune to all isolates except for two which were placed in group VII. Group VII isolates infected all "resistant" cultivars tested, including PI 96.983 and 'Tokyo'. The symptoms of group VII infection of Buffalo were severe systemic necrosis and bud blight about 2 to 3 weeks after inoculation. Group VII isolates infecting susceptible soybean cultivars such as Rampage and 'Clark 63' cause typical mosaic symptoms that are difficult to differentiate from the symptoms caused by group I isolates which infected none of the resistant cultivars. (It may be of interest to note that when Buffalo is inoculated with group VII isolates only about half the plants become infected. Reinoculation results in infection of all of the previously noninfected plants. Buffalo thus does not appear to possess any immunity to group VII isolates but it is difficult to inoculate.)

We have conducted less exhaustive tests with PI 96.983. Our results show, however, that this line, like Buffalo, also has a high degree of resistance to many SMV isolates. PI 96.893 is susceptible to the group VII isolates and also to a seedborne isolate (ISP-29) isolated by R. M. Goodman in 1975 from 'Calland' soybeans grown at Seville, Spain, to which Buffalo is immune.

Buffalo is a late maturing variety (group VIII) and has a desirable growth habit and other agronomic characteristics which, in combination with its immunity to all but the most virulent of SMV isolates, will be of particular interest to breeders who require a tropically adapted source of SMV resistance. We have tested the cultivars 'Geduld' and 'Hernon 147', the parents of Buffalo, kindly supplied to us by Dr. J. R. Tattersfield, Crop Breeding Institute, P.O. Box 8100, Causeway, Salisbury, Rhodesia. Geduld was susceptible to SMV-

Il-S but Hernon 147 was immune. No tests with other more virulent SMV isolates have been conducted to date on these parental cultivars. We are now engaged in a genetic study to determine the inheritance of Buffalo's SMV resistance and to incorporate this trait into advanced, tropically adapted soybean cultivars (unpublished work of Glenn R. Bowers, Jr., E. H. Paschal II, and R. M. Goodman).

Several F_1 plants of the cross Buffalo x 'Jupiter' were inoculated with SMV-Il-S in the field in Puerto Rico in June, 1977. The plants were inoculated twice, once at the primary leaf stage and again 2 weeks later. We have found Jupiter to be susceptible to the SMV isolate used in this study. The F_1 plants remained symptomless throughout the growing season. It appears, therefore, that the Buffalo source of SMV resistance is controlled by one or more dominant genes.

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1) Additional sterile and male sterile mutants in soybean.

In the M_2 populations of different soybean varieties irradiated with gamma rays, a total of seven lines showed segregation for sterility at maturity. The detailed genetic and cytogenetic studies of these lines were conducted in M_3 and M_4 populations derived from fertile segregates of the M_2 progenies. Four of these were found to be both male and female sterile, whereas, three of these showed female fertility but male sterility as indicated below (Table 1).

Morphological appearance: The sterile segregates in all these lines were identical to fertile segregates until the onset of flowering. As it has been reported by several workers, the sterile plants showed proliferation of vestigial pods at the flowering nodes and the leaves looked dark green and leathery and remained attached to the stem. No pod setting was observed in PK-71-39 S-1, PK-71-39 S-2, Ankur S-1 and Bragg S-1. Whereas, the sterile plants of UPSM-229 MS-1, UPSM-229 MS-2 and UPSL-18 MS-1 had varying number of pods as indicated in Table 2. UPSL-18 MS-1 appeared to set maximum number of pods.

Inheritance: The inheritance of sterility/male sterility in all these lines was monogenic with sterility/male sterility being the recessive trait.

Table 1

Lines used in the study

Lines	Dose of gamma rays	Nature of sterility
PK-71-39 S-1	10 kr	Complete male and female sterility
PK-71-39 S-2	10 kr	Complete male and female sterility
Ankur S-1	10 kr	Complete male and female sterility
Bragg S-1	10 kr	Complete male and female sterility
UPSM-229 MS-1	10 kr	Complete male sterility and partial female fertility
UPSM-229 MS-2	10 kr	Complete male sterility and partial female fertility
UPSL-18 MS-1	20 kr	Partial male sterility and complete female fertility

Table 2

Number of pods/plant and number of seeds/pod in UPSM-229 MS-1, UPSM-229 MS-2 and UPSL-18 MS-1 lines

Male sterile lines	No. of pods/plant				No. of seeds/pod	
	Sterile plant		Fertile plant			
	Mean	Range	Mean	Range	Sterile plant	Fertile plant
UPSM-229 MS-1	0.78	1-6	83.34	40-162	1.00	2.46
UPSM-229 MS-2	0.86	1-7	89.55	39-173	1.00	2.59
UPSL-18 MS-1	32.27	7-60	67.76	45-101	1.15	2.11

However, the interline crosses have not been studied so far to elucidate the allelic relationship among these lines.

Pollen characteristics: Striking differences were observed between the pollen produced on the sterile and fertile plants of these lines. The proportion of stained and unstained pollen grains as well as the data on the pollen size for fertile and sterile plants of seven lines are presented in Table 3.

Table 3

Pollen characteristics in fertile and sterile plants

Male sterile line	Percentage of stained pollen		Size of stained pollen (in micron)				Size of unstained pollen (in micron)			
			Sterile		Fertile		Sterile		Fertile	
	Sterile	Fertile	Mean	Range	Mean	Range	Mean	Range	Mean	Range
PK-71-39 S-1	9.09	98.20	24.20	20-30	21.17	20-24	17.44	6-30	19.50	19-20
PK-71-39 S-2	19.49	98.00	22.52	16-30	21.32	20-24	16.23	7-25	20.00	19-20
Ankur S-1	3.64	99.00	27.50	25-30	20.79	20-24	16.10	6-22	21.00	20-22
Bragg S-1	3.77	99.10	24.75	24-25	23.24	20-27	16.77	10-23	20.00	19-21
UPSM-229 MS-1	67.25	98.00	28.77	25-38	20.92	20-25	17.29	10-25	20.50	20-21
UPSM-229 MS-2	93.00	98.50	47.90	40-50	20.75	20-25	33.14	30-40	20.50	20-21
UPSL-18 MS-1	75.00	99.00	25.09	10-35	25.60	22-30	25.24	10-30	20.00	19-21

Pollen grains produced on the sterile plants of PK-71-39 S-1, PK-71-39 S-2, Ankur S-1 and Bragg S-1 had less percentage of stained pollen in comparison with the pollen grains produced on the corresponding normal plants. Higher percentage of stained pollen was observed in the male sterile plants of UPSM-229 MS-1, UPSM-229 MS-2 and UPSL-18 MS-1. The mean percentage of stained pollen was 67.25% in UPSM-229 MS-1, 93% in UPSM-229 MS-2 and 75% in UPSL-18 MS-1.

Unstained pollen grains produced on sterile plants of all these lines had diameter of variable sizes. Unstained pollen grains derived from the sterile plants of PK-71-39 S-1, PK-71-39 S-2, Ankur S-1 and UPSL-18 MS-1 had variable sizes in the range of 6μ to 30μ, 7μ to 25μ, 6μ to 22μ and 10μ to 30μ, respectively. However, the unstained pollen derived from sterile plants of Bragg S-1, UPSM-229 MS-1 and UPSM-229 MS-2 had less variability in size ranging from 10μ to 23μ, 10μ to 25μ and 30μ to 40μ, respectively. A very narrow range of size variability was observed for the unstained pollen produced on the fertile plants of all sterile lines. Among the unstained pollen derived from the sterile plants of PK-71-39 S-1, PK-71-39 S-2, Ankur S-1, Bragg S-1 and UPSM-229 MS-1, no significant difference was noticed for their mean size. But the mean size of unstained pollen produced on the sterile plants of UPSL-18 MS-1 (25.24μ) and UPSM-229 MS-2 (33.14μ) was significantly greater than the rest of the sterile lines.

No difference was observed for size between the stained pollen produced on the sterile plants and stained pollen produced on the fertile plants of UPSL-18 MS-1. It had 75% stained pollen.

The stained pollen produced on the sterile plants of UPSM-229 MS-2 had the mean diameter of 47.90μ, which was more than twice the mean diameter (20.75μ) of the stained pollen produced on the fertile plants of UPSM-229 MS-2.

Cytological behavior: Meiotic studies indicated that sterility in case of PK-71-39 S-1 and PK-71-39 S-2 was due to asynapsis as evident from the presence of 40 univalents during diakinesis. In PK-71-39 S-1 the univalents were clumped in the center at metaphase I, whereas these were scattered around the equatorial plate in the case of PK-71-39 S-2. Irregular distribution of chromosomes and the presence of laggards during anaphase I led to the formation of 2 to 5 microspores in a sporad, which finally gave rise to varying sizes of unstained pollen grains.

In Ankur S-1, desynapsis appeared to be the cause of sterility. In early as well as mid-prophase stages, most of the pollen mother cells showed

20 bivalents. However, varying numbers of chromosomes were observed during diakinesis indicating several univalents. The subsequent abnormalities were similar to those of PK-71-39 S-1 and PK-71-39 S-2.

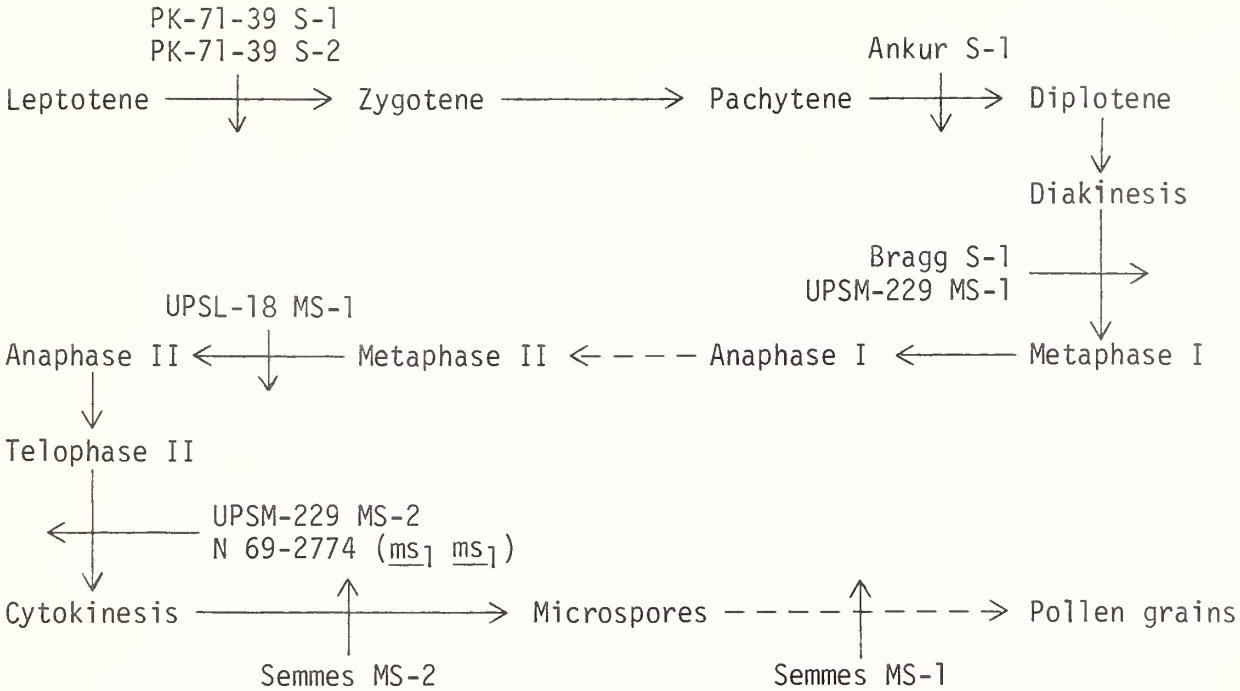
The sterility in Bragg S-1 was due to abnormal metaphase I. Normal bivalents were observed up to diakinesis stage but they failed to align properly on the equatorial plate at metaphase I. Consequently these bivalents did not engage spindle fibers, leading to unequal and random distribution of chromosomes at anaphase I. Thus, after anaphase II the resulting sporads had 3 to 6 microspores per sporad, giving rise to varying size pollen grains.

Sterility in UPSM-229 MS-1 was also due to absence of proper alignment of bivalents at metaphase I. At anaphase I, two unequal groups of chromosomes could be seen with no laggards in the center indicating unequal distribution of bivalents at anaphase I. Furthermore, the arrangement of four nuclei at anaphase II was not isobilateral. The sporads had two to four microspores per sporad, with the frequency of dyads maximum.

There was no cytokinesis in UPSM-229 MS-2, and due to which no microspores were formed. The pollen mother cells themselves gave rise to single large size pollen having all the four daughter nuclei.

In case of UPSL-18 MS-1, meiosis was normal up to metaphase II, but the anaphase II appeared to be abnormal. Instead of the chromatids going to different poles they remained together even at the end of anaphase II, giving rise to mostly dyads after telophase II.

The mutants studied in the present investigation and the male sterile mutants studied by Patil and Singh (1975) viz. Semmes MS-1, Semmes MS-2 and N 69-2774 show a definite relationship between a particular mutation and a particular step during sporogenesis. Invariably, the cytological abnormality in each line studied was always restricted to only one step in the process of pollen formation. From the genetic studies, it has been clearly established that the sterility/male sterility and the cytological abnormality in each line is under monogenic control. The different steps being affected by the mutant genes during sporogenesis can be summarized as follows:



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1) Glyceride structure variation in soybean varieties.

The glyceride structure of an oil, i.e., the combinations of fatty acids that occur together in the triglycerides, may influence its stability to oxidation (Raghuveer and Hammond, 1967). Recently we examined the glyceride structure of about 20 varieties of soybean and related species by two techniques: stereospecific analysis and silver ion chromatography (Fatemi and Hammond, 1977a, 1977b). Stereospecific analysis measures the proportion of each fatty acid on each of the three positions of glycerol. The second technique, silver ion chromatography, partly resolves the triglycerides of an oil according to the number of double bonds per molecule.

The glyceride structure variation that occurred from year to year for several varieties was very small when the soybeans were grown at one location.

The soybeans were chosen to embrace a wide range of fatty acid compositions. To make comparisons of the stereospecific analyses, we plotted the percentage of a fatty acid on one of the three glycerol positions versus the percentage of this fatty acid in the whole fat. This has been shown to give straight lines as in Fig. 1. Similar plots were obtained for the other fatty acids in soybean oil. No one knows how the glyceride structure of oils is controlled, but we reasoned that samples falling on the lines probably were controlled by the same mechanism. If there were genetic variation in the mechanism controlling glyceride structure, it would likely appear as a deviation from the linear relation. One deviant, PI 68.788, is shown in Fig. 1. A sample of Glycine gracilis also seemed to deviate from the lines for Glycine max in the distribution of linolenic acid.

Attempts have been made to predict the amounts of individual triglycerides assuming that random combinations of fatty acids occur with the single restraint that the proportion of each fatty acid on the three glycerol positions must conform to the stereospecific analysis. The groups of triglycerides resolved by the silver ion technique were compared with values calculated by this theory from the stereospecific analysis. In general the agreement was close, but triglycerides that contained two or more oleic or linoleic acids were in amounts greater than predicted while combinations that contained both oleic and linoleic acids were in slightly lesser amounts than predicted. This may be because during ripening, the fatty acid composition of soybeans changes considerably, and the maxima for oleic and linoleic acids do not coincide in time (Fehr et al., 1971). This would depress combinations of the two acids and favor multiple occurrence of one acid on the same molecule.

Plots of the amounts of the triglyceride groups obtained by silver ion analysis versus the percentage in the whole oil of one of their constituent fatty acids revealed regular but nonlinear relations. PI 68.788 was a frequent deviant in these plots also. No other significant deviations were discovered.

The two procedures that we used are too complex to use in screening soybean varieties for deviant glyceride structures, but it is possible to determine the percentages of fatty acids on the 2-position of glycerol and the mixed 1- and 3-positions rather simply by an enzymatic hydrolysis with pancreatic lipase. We believe this would make a feasible analytic method for a screening test.

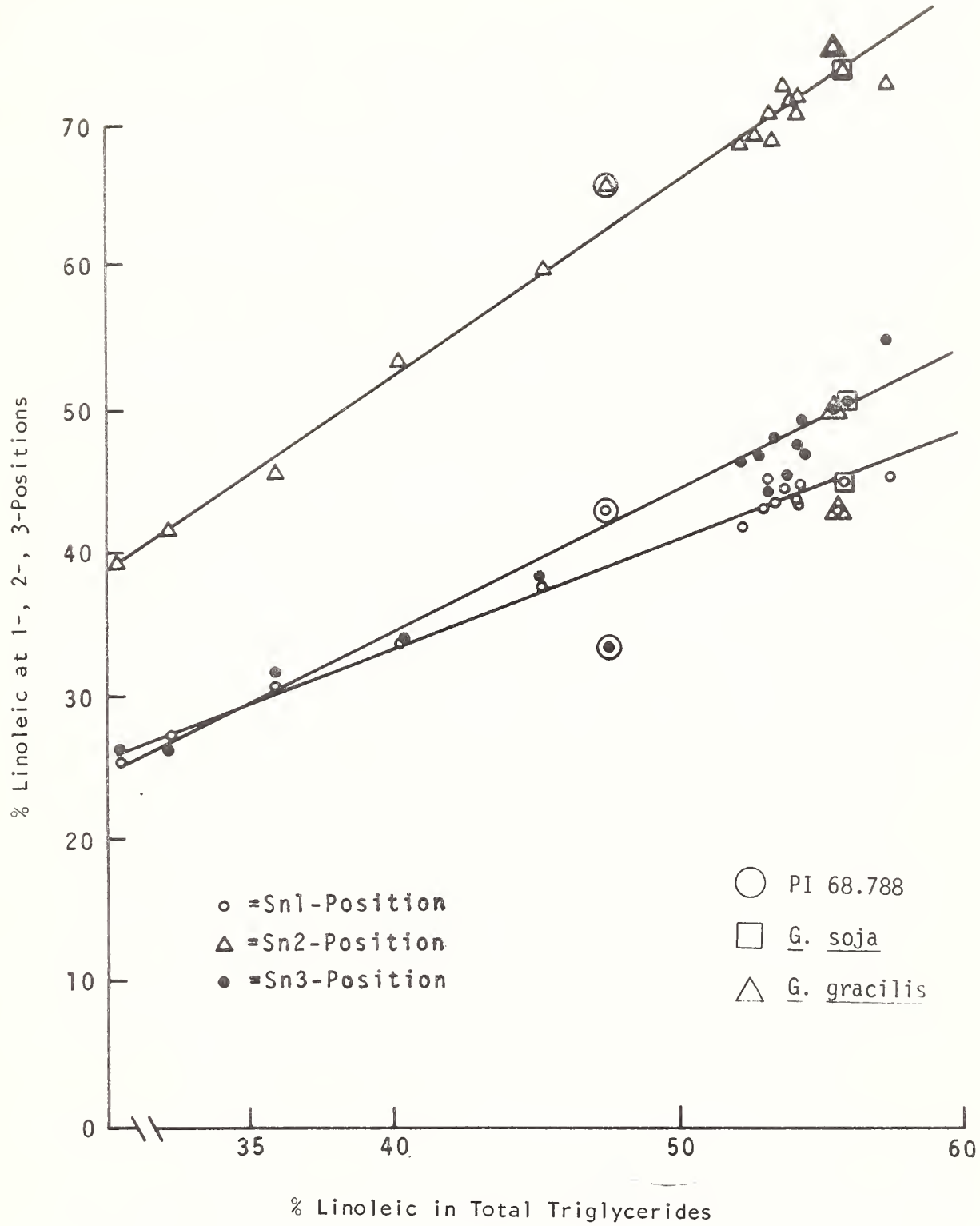

Fig. 1. Distribution of linoleic acid among the 1-, 2-, and 3-positions against changes in the percentage of linoleic acid in the total triglycerides

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1) Evidence for linkage of G with one of the B loci in soybeans.

In 1963, Tang and Li reported on a study of a cross, Glycine max x G. formosana (G. formosana = G. soja), in which the inheritance of a number of qualitative traits was determined. This paper is a reinterpretation of a portion of their data.

Among the genes segregating in the cross were the following:

$\underline{i}^{i}/\underline{i}$: restriction of dark seedcoat pigments to hilum/self-dark seed

G/g: green seedcoat/yellow seedcoat (obscured in ii genotypes)

$B_2, B_3/b_2, b_3$: two of the three complementary factors for bloom on seedcoat; in the cross studied, both parents were B_1B_1, so that segregation at the other two loci produced F_2 ratios of 9 bloom : 7 smooth.

Parental genotypes were $\underline{i}^{i}\underline{i}^{i}ggb_2b_2b_3b_3$ for G. max and $iiGGB_2B_2B_3B_3$ for G. soja. When F_2 plants were classified as to seed color (green, yellow, black) and presence or absence of bloom, the observed numbers gave a poor fit (χ^2 probability 0.006) to the ratio expected under independent inheritance. Taken singly, the characters fit the appropriate monogenic and digenic ratios well. Thus, linkage is suspected. The data are consistent with the hypothesis of independent segregation of $\underline{i}^{i}/\underline{i}$ and G/g, and of $\underline{i}^{i}/\underline{i}$ and the genes controlling

bloom. There remain for consideration the totals for the combinations of $\underline{G}/\underline{g}$ vs $\underline{B}_2\text{-}\underline{B}_3\text{-}/\underline{b}_2\underline{b}_2\underline{b}_3\underline{b}_3$, as follows:

Phenotype	Observed number	Number expected given independence
bloom-green	125	104.6
smooth-green	57	81.4
bloom-yellow	31	34.9
smooth-yellow	35	27.1

The χ^2 probability for these totals, given independent inheritance, is 0.003, and a deficiency of recombinant classes is apparent. Calculation of linkage intensity is complicated by the complementary action of the $\underline{B}_2$ and $\underline{B}_3$ genes. Presumably one, say $\underline{B}_3$, is linked to $\underline{G}$, while the other is independent. We can use the maximum likelihood method, described by Mather (1946), to calculate linkage intensity. With p = the frequency of coupling type gametes ($\underline{B}_3\underline{G} + \underline{b}_3\underline{g}$), we can derive m_c, the expected frequency of each phenotypic class. There are eight types of gametes produced by the F_1 plant: (1) $\underline{B}_2\underline{B}_3\underline{G}$; (2) $\underline{b}_2\underline{B}_3\underline{G}$; (3) $\underline{B}_2\underline{b}_3\underline{g}$; (4) $\underline{b}_2\underline{b}_3\underline{g}$; (5) $\underline{B}_2\underline{B}_3\underline{g}$; (6) $\underline{b}_2\underline{B}_3\underline{g}$; (7) $\underline{B}_2\underline{b}_3\underline{G}$; and (8) $\underline{b}_2\underline{b}_3\underline{G}$. Each of the first four occurs with frequency $\frac{1}{4}p$, the other four with frequency $\frac{1}{4}(1\text{-}p)$. The smooth yellow phenotype, for example, is produced by the following gametic combinations:

Female gamete	Male gamete	Frequency
B_2b_3g	B_2b_3g	$(\frac{1}{4}p)^2$
B_2b_3g	b_2b_3g	$(\frac{1}{4}p)^2$
b_2b_3g	B_2b_3g	$(\frac{1}{4}p)^2$
b_2b_3g	b_2b_3g	$(\frac{1}{4}p)^2$
b_2b_3g	b_2B_3g	$(\frac{1}{4}p)(\frac{1}{4})(1\text{-}p)$
b_2B_3g	b_2b_3g	$(\frac{1}{4}p)(\frac{1}{4})(1\text{-}p)$
b_2B_3g	b_2B_3g	$(\frac{1}{4}[1\text{-}p])^2$

The sum of the frequencies of individual gametic combinations yields the value of m_c for each class. The values are as follows:

Phenotype	m_c	Observed number
bloom – green	$\frac{3(2+p^2)}{16}$	a
smooth – green	$\frac{3(2-p^2)}{16}$	b
bloom – yellow	$\frac{3(1-p^2)}{16}$	c
smooth – yellow	$\frac{3p^2+1}{16}$	d

The likelihood expression, to be maximized with respect to p, is

$$P(a,b,c,d|p) = \frac{n!}{a!b!c!d!}\left[\frac{3(2+p^2)}{16}\right]^a\left[\frac{3(2-p^2)}{16}\right]^b\left[\frac{3(1-p^2)}{16}\right]^c\left[\frac{3p^2+1}{16}\right]^d ,$$

where $n = a+b+c+d$. Taking the logarithm before differentiating, this becomes

$$\frac{d\ \ln P}{dp} = \left(\frac{a}{2+p^2} - \frac{b}{2-p^2} - \frac{c}{1-p^2} + \frac{3d}{1+3p^2}\right)(2p) .$$

This expression is now set equal to zero, and, with $p^2 = x$, becomes, after simplification

$$3(a+b+c+d)x^3 + (-8a+4b+c-3d)x^2 + (3a-5b-12c-12d)x + (2a-2b-4c+12d) = 0.$$

Now the observed values 125, 57, 31, and 35 are substituted for a, b, c, and d, respectively, and the equation (which has only one solution between 0 and 1) is solved by successive approximation to get $x = p^2 = 0.462466$. Thus, $p = 0.680$, and the recombination frequency, 1-p, is 0.320.

The standard error, s_p, of the calculated recombination frequency is determined using the information concept described by Mather (1946). The formulas are

$$i_c = \left(\frac{1}{m_c}\right)\left(\frac{dm_c}{dp}\right)^2 , \quad I_p = \sum_c i_c , \quad \text{and} \quad s_p = \sqrt{\frac{1}{nI_p}} .$$

Here, $s_p = 0.053$.

Weiss (1970) assigned G/g to Linkage Group 3. Further studies should be carried out in an attempt to verify the loose linkage between G/g and either B_2/b_2 or B_3/b_3 for which evidence has been given.

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2) Soybean linkage tests.

F_2 linkage results are presented in Table 1 with a = XY, b = Xy, c = xY and d = xy for the gene pairs listed in the form of Xx and Yy. Percentage recombination was obtained from the ratio of products following the method of Immer and Henderson (1943).

Results from testing F_3 seeds and seedlings to determine F_2 phenotypes indicate possible linkage between seed coat peroxidase (ep) and root fluorescence (fr). Further studies are in progress to test this hypothesis. All other combinations were inherited independently.

Table 1

F_2 linkage tests

Genes	General phenotypic classes a	b	c	d	Sum	%R ± SE	Linkage phase
			'Minsoy' (T_1 fr ep Pb) x 'Hark' (t_1 Fr Ep pb)				
Pb pb Fr fr	235	89	71	25	420	49.0 ± 3.7	repulsion
Pb pb T_1 t_1	255	96	79	25	455	52.4 ± 3.6	coupling
Pb pb Ep ep	267	81	75	24	447	50.7 ± 3.5	repulsion
Fr fr T_1 t_1	226	81	78	35	420	53.1 ± 3.5	repulsion
Fr fr Ep ep	240	62	76	36	414	41.6 ± 3.3	coupling
			(Ep T_1 w_1 F) x (ep t_1 W_1 f)				
W_1 w_1 F f	738	191	252	71	1252	51.2 ± 2.1	repulsion
Ep ep T_1 t_1	418	123	139	33	713	53.0 ± 2.9	coupling
Ep ep W_1 w_1	393	112	141	32	713	46.8 ± 3.0	repulsion

Table 1 (cont'd)

Genes	General phenotypic classes a	b	c	d	Sum	%R ± SE	Linkage phase
			($\underline{Ep}$ $\underline{T_1}$ $\underline{w_1}$ $\underline{F}$) x ($\underline{ep}$ $\underline{t_1}$ $\underline{W_1}$ $\underline{f}$) (cont'd)				
$\underline{Ep}$ $\underline{ep}$ $\underline{F}$ $\underline{f}$	440	120	117	36	713	48.3 ± 2.8	coupling
$\underline{T_1}$ $\underline{t_1}$ $\underline{W_1}$ $\underline{w_1}$	704	233	225	90	1252	52.7 ± 2.1	repulsion
$\underline{T_1}$ $\underline{t_1}$ $\underline{F}$ $\underline{f}$	773	254	266	76	1369	52.0 ± 1.4	coupling
			(Separate crosses)				
$\underline{T_1}$ $\underline{t_1}$ $\underline{Ep}$ $\underline{ep}$	258	69	84	36	447	> 55.0	repulsion
$\underline{L_1}$ $\underline{l_1}$ $\underline{K_2}$ $\underline{k_2}$	113	48	39	12	212	54.5 ± 5.4	coupling
$\underline{K_2}$ $\underline{k_2}$ $\underline{T_1}$ $\underline{t_1}$	374	125	119	39	657	49.8 ± 2.9	repulsion
$\underline{L_1}$ $\underline{l_1}$ $\underline{T_1}$ $\underline{t_1}$	165	26	37	8	236	54.4 ± 4.6	repulsion

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3) A possible cytoplasmic mutant.

A chimera plant (A75-1165-117) was observed in 1975 in the F_2 of a cross of Ames $\underline{ms_1}$ x 'Clark' homozygous translocation (Table 1). Reciprocal crosses were made with 'Clark 63', using branches from the chimera plant that contained a high percentage of yellow trifoliolates. Selfed seed of the chimera plant (A75-1165-117) and F_1 seed from reciprocal crosses were planted in the field in 1976 (Table 2).

We observed 36 yellow and 17 green seedlings from self-pollination of the chimera plant. Twenty-seven yellow and 3 green plants were killed in a June hail storm. The yellow plants segregated for the translocation and gave all yellow plants in the F_4 and F_5. The green plants segregated for the translocation and 13 gave all green plants in the F_4 and F_5. One green plant, however, was lightly chimeric and in the F_4 segregated 198 green : 13 yellow plants.

Table 1

Pedigree of chimera plant A75-1165-117

A72-T30	Ames $\underline{ms}_1$ (See Soybean Genet. Newsl. 1: 28-30, 1974, and Soybean Genet. Newsl. 2: 16-18, 1975)
A73g-13	F_1 plant (A72-T30 $\underline{ms}_1$ x Clark 63)
A73-131	F_2 segregated 3 fertile : 1 sterile
A74-144	F_1 plant (A73-131-15 $\underline{ms}_1$ x Clark homozygous translocation from *G. soja* PI 101.404B)
A75-1165	F_2 segregated for both $\underline{ms}_1$ and translocation; plant 117 was a chimera and heterozygous for translocation

At present, 84 green F_4 plants have been progeny tested and all 2539 F_5 seedlings were green. One yellow F_4 plant has been progeny tested and gave all yellow F_5 seedlings (Table 2).

When the chimera plant was female parent with Clark 63, we observed 9 yellow and 1 green F_1 seedlings. Eight yellow seedlings were killed in the hail storm. In the F_2, progeny of the yellow F_1 plant segregated for the translocation and gave all yellow progeny, and progeny of the green F_1 plant segregated for the translocation and gave all green progeny. Since we were using chimera branches for pollinations, we assumed that the green F_1 plant did not receive the factor for yellow plant color in the female gamete because we did not observe yellow plants in the F_2 (Table 2).

When the chimera plant was male parent with Clark 63, we observed 23 green F_1 seedlings. Seven seedlings were killed in the hail storm. In the F_2 the green F_1 plants segregated for the translocation, but gave all green progeny. The absence of segregation in the F_2 suggests that cytoplasmic inheritance is involved.

In the crosses with A75-1165-117 we could not tell if the "hybrids" were cross-pollinations or self-pollinations because we had no genetic markers to observe for segregation (Table 2). Yellow plant color may or may not be carried in the gametes because we were crossing with chimeric branches.

In 1977, progeny from the lightly chimeric F_3 plant segregated 198 green : 13 yellow plants. Although this segregation approximated a 15 : 1 ratio, data

Table 2

Evaluation of selfed progeny and crosses with yellow plants derived from self-pollination of A75-1165-117

Parents	F_3 generation	F_4 generation	F_5 generation
Self-pollination of F_2 plant A75-1165-117	36 yellow plants (27 died)	5 F_3 plants segregated for translocation and gave all yellow progeny (73 plants)	6 F_4 plants gave all yellow progeny (152 plants)
		4 F_3 plants did not segregate for translocation and gave all yellow progeny (66 plants)	10 F_4 plants gave all yellow progeny (250 plants)
	17 green plants (3 died)	6 F_3 plants segregated for translocation and gave all green progeny (736 plants)	
		7 F_3 plants did not segregate for translocation and gave all green progeny (931 plants)	
		1 F_3 plant did not segregate for translocation and was lightly chimeric and segregated as follows:	
		- 198 green plants	84 F_4 plants gave all green progeny (2539 plants)
		- 13 yellow plants	1 F_4 plant gave all yellow progeny (21 plants)

Table 2 (cont'd)

Parents	F_1 generation	F_2 generation
A75-1165-117 x Clark 63	9 yellow plants (8 died)	1 F_1 plant segregated for translocation and gave all yellow progeny (4 plants)
	1 green plant	1 F_1 plant segregated for translocation and gave all green progeny (218 plants)
Clark 63 x A75-1165-117	23 green plants (7 died)	10 F_1 plants segregated for translocation and gave all green progeny (961 plants)
		6 F_1 plants did not segregate for translocation and gave all green progeny (887 plants)

collected previously suggested cytoplasmic inheritance; data collected subsequently substantiated the hypothesis of cytoplasmic inheritance. The chimeric condition of the F_3 plant was reflected in the F_4 segregation.

Allelism testcrosses and their reciprocals were made between the new yellow mutant and other yellow mutants ($\underline{y}_9$, $\underline{y}_{10}$, $\underline{Y}_{11}\underline{y}_{11}$, $\underline{y}_{12}$, $\underline{y}_{13}$, $\underline{Y}_{18}$ – and T253). All F_1 progeny behaved as expected if the new yellow mutant was inherited cytoplasmically.

In Table 3, we have presented parental, F_1 and F_2 data for reciprocal crosses with $\underline{Y}_{18}$ $\underline{Y}_{18}$. We have $\underline{w}_1$ as a nuclear genetic marker from $\underline{Y}_{18}$. The data indicate that the new yellow plant trait is inherited cytoplasmically.

Table 3

Evaluation of F_1 and F_2 generations of reciprocal crosses with yellow plants derived from self-pollination of A75-1165-117

Parents	F_1 generation	F_2 generation
$\underline{Y}_{18}$ $\underline{Y}_{18}$ $\underline{w}_1$ $\underline{w}_1$ x yellow $\underline{W}_1$ $\underline{W}_1$	green $\underline{W}_1$	131 green $\underline{W}_1$: 41 green $\underline{w}_1$
yellow $\underline{W}_1$ $\underline{W}_1$ x $\underline{Y}_{18}$ $\underline{Y}_{18}$ $\underline{w}_1$ $\underline{w}_1$	yellow $\underline{W}_1$	126 yellow $\underline{W}_1$: 44 yellow $\underline{w}_1$

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1) Genetic linkage studies of factors controlling nitrogen fixation.

We are especially concerned with the genetic factors controlling symbiotic nitrogen fixation in soybeans. Four classical Mendelian factors have been identified in the macrosymbiont which regulate nodulation response (Vest et al., 1972). These are: $\underline{rj}_1$, which in homozygous recessive condition produces a non-nodulating phenotype with a broad spectrum of Rhizobium strains (Williams and Lynch, 1954); $\underline{Rj}_2$, a dominant factor conditioning an ineffective response with strains of the C1 and 122 serogroups (Caldwell, 1966); $\underline{Rj}_3$,

a factor conditioning an ineffective response with strain 33 (Vest, 1970); and $\underline{Rj}_4$, also a dominant factor, conditioning an ineffective response with strain 61 (Vest and Caldwell, 1972). Crosses have been made with a number of genetic markers for each of these Rj factors in a search for their respective linkage associations. Genetic markers were selected where possible on the basis of:

a) known association with linkage groups,

b) unambiguous phenotypic classification, and

c) phenotypic expression in the seedling stage.

As an initial step in this long-term effort at determining the linkage association of the Rj factors, we present data (Table 1) from two crosses evaluated in the field at Beltsville during the summer of 1977. T lines were obtained from the Soybean Genetic Type Collection maintained by R. L. Bernard (Bernard and Weiss, 1973). Parental genotypes were crossed in the field at Beltsville in 1975.

Table 1

Soybean linkage test

Genes	a	b	c	d	Sum	%R	SE	Phase
	Clark ($\underline{rj}_1$ $\underline{rj}_1$ Ln Ln) x T41 ($\underline{Rj}_1$ $\underline{Rj}_1$ ln ln)							
$\underline{Rj}_1$ $\underline{rj}_1$ Ln ln	107	28	24	14	173	I	--	R
	T145 ($\underline{Rj}_1$ $\underline{Rj}_1$ P P) x Clark ($\underline{rj}_1$ $\underline{rj}_1$ p p)							
$\underline{Rj}_1$ $\underline{rj}_1$ P p	115	33	34	9	191	51	5.4	C

The F_1 hybrids were advanced to the F_2 generation in the greenhouse during the winter 1975-76. Several hundred F_2 plants were grown in the field at Beltsville in 1976 and F_3 seed was harvested from individual plants. In 1977, 100 F_3 seed were planted in each progeny row in a field at Beltsville known to produce well-nodulated plants with commercial soybean lines. All plants were dug and classified for nodulation response and other characters. F_2 genotypes were rationalized from the F_3 progeny test. The recombination percentage was calculated by the product method as described by Immer and Henderson (1943). These results indicate independent assortment of $\underline{rj}_1$ with ln (narrow leaf) and P (glabrous).

We have also evaluated the possible linkage of $\underline{Rj_4}$ and $\underline{P}$. Hybridization and generation advance followed the procedures previously described. However, since the $\underline{Rj_4}$ phenotype is distinguishable only when the plants are subject to infection exclusively with Rhizobium japonicum strain 61, the F_3 progeny were seeded in the greenhouse in the growth tray assemblies described by Devine and Reisinger (1977) and inoculated with 7-day-old broth cultures of strain 61 of the Beltsville Culture Collection. Approximately 45 seed were planted for each F_3 line. Three to four weeks after seeding, the plants were dug from the vermiculite growth media and scored for nodulation type and pubescence. The results (Table 2) indicate a positive linkage association of $\underline{Rj_4}$ and $\underline{p}$. To our knowledge this is the first documented report of a linkage association of a factor controlling symbiotic nitrogen fixation in soybeans. Larger populations are being assayed to obtain a more precise estimate of the genetic map units separating these loci.

Reasoning from the positive linkage association of $\underline{Rj_4}$ and $\underline{P}$ demonstrated in Table 2 and from the lack of linkage of $\underline{rj_1}$ with $\underline{P}$ (Table 1), we conclude that $\underline{Rj_4}$ and $\underline{rj_1}$ are not allelic.

Table 2

Soybean linkage tests

Genes	a	b	c	d	Sum	%R	SE	Phase
Hill ($\underline{Rj_4}$ $\underline{Rj_4}$ $\underline{p}$ $\underline{p}$) x T145 ($\underline{rj_4}$ $\underline{rj_4}$ $\underline{P}$ $\underline{P}$)								
$\underline{Rj_4}$ $\underline{rj_4}$ $\underline{P}$ $\underline{p}$	60	32	24	2	118	2.6	8.5	R

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1) Evaluation of soybean germplasm for resistance to corn earworm--I.*

Corn earworm (Heliothis zea Boddie) is one of the most destructive pests of soybeans (Glycine max [L.] Merr.) and its infestation sometimes can cause complete crop loss (Turnipseed, 1973). This pest feeds on both the foliage and developing seeds in the pods. Soybeans become primary host as corn and cotton become more mature and consequently less attractive for oviposition (Freeman et al., 1967). Each larva is capable of damaging 6 to 8.2 pods and 7.1 seeds between 4th and 6th instars, both inclusive (Boldt et al., 1975; Smith and Bass, 1972). The objective of the present investigation was to identify germplasm resistant to this pest.

One hundred seventy-four cultivars belonging to Maturity Groups 00-IV were planted in three replications in the screen house (108'x72'x15') during 1974. Ten seeds of each cultivar were sown on May 14, the seeds being 2" apart within the row and rows being 36" apart. Screen house was infested by releasing 2,244 corn earworm moths. The moth releases were started on June 26 and continued until September 23. Plants were harvested at maturity and the number of undamaged and damaged pods was recorded for each cultivar. Data were analyzed statistically by employing ANOVA; Duncan's Multiple Range Test was used to test significant difference between the means.

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*This is part of a CSRS/USDA funded project.

The mean numbers of undamaged and damaged pods/plant for each cultivar are given below. (Means which are not followed by the same letter are significantly different at the 0.05 probability level.)

Table 1
Mean number of undamaged and damaged pods
for different soybean cultivars

Cultivar	Undamaged pods	Damaged pods	Cultivar	Undamaged pods	Damaged pods
		Maturity Group 00			
Norman	2.7a	1.1a	Ogemaw	5.2a	2.5a
Morsoy	3.0a	2.7a	Altona	5.4a	3.0a
Pagoda	3.0a	2.5a	Ada	5.6a	5.9b
Crest	3.9a	0.7a	Flambeau	5.7a	2.0a
Hidatsa	4.0a	2.0a	Manitoba Brown	5.8a	2.3a
Acme	4.8a	0.7a	Agate	6.4a	1.6a
Pando	4.9a	5.0b			
		Maturity Group 0			
Norchief	1.9a	3.3a	Hardome	4.7a	1.6a
Goldsoy	2.6a	1.1a	Merit	5.7a	2.2a
Capital	3.6a	5.6a	Grant	8.8a	5.5a
Mandarin Ottawa	4.1a	3.9a	Kabott	11.5a	3.8a
Poland Yellow	4.6a	2.7a			
		Maturity Group I			
Manchuria	0.2a	1.3ab	Pridesoy	4.3ab	2.2a-c
Portugal	1.5ab	1.7a-c	Chippewa 64	5.4ab	2.1a-c
Harly	1.8ab	0.2a	EarlyAna	5.5ab	1.4a-c
Norsoy	1.9ab	1.8a-c	Cayuga	6.1a-c	0.4a
Ontario	2.4ab	1.6a-c	Manchu Montreal	6.2a-c	3.5a-c
Rampage	2.4ab	1.2ab	Ottawa	6.3a-c	2.9a-c
Renville	2.7ab	0.9ab	Mandarin	6.5a-c	4.7bc
Giant Green	2.8ab	0.1a	OAC 211	9.2a-d	3.2a-c
SRF 150	3.0ab	1.3ab	A-100	9.3a-d	3.2a-c
Anoka	3.1ab	1.9a-c	Bombay	10.5b-d	1.5a-c
Blackeye	3.2ab	1.2ab	Kagon	10.9b-d	4.0a-c
Medium Green	3.2ab	1.6a-c	Blackhawk	11.0b-d	2.3a-c
Burwell	3.5ab	1.4a-c	Elton	11.3b-d	1.4a-c
Monroe	3.5ab	3.2a-c	Chippewa	15.5cd	7.4c
Mendota	3.6ab	1.5a-c	Hoosier	15.6cd	6.5bc
Hark	3.7ab	0.7ab	Disoy	17.2d	5.4a-c

Table 1 (cont'd)

Cultivar	Undamaged pods	Damaged pods	Cultivar	Undamaged pods	Damaged pods
		Maturity Group II			
Henry	2.6a	0.1a	Zinman 533	6.9ab	5.6cd
Goku	2.7a	0.4a	Manchu 606 Wis.	7.0ab	7.4de
Bansei (Ames)	4.6ab	0.6a	Manchu Kota	7.1ab	2.3a-c
Manchu 3 Wis.	5.1ab	2.6a-c	Lindarin	7.2ab	2.1a-c
Magna	5.4ab	1.6a-c	Prize	7.4ab	2.9a-c
Madison	5.8ab	2.1a-c	Bansei	7.8ab	0.3a
Harwood	6.0ab	2.1a-c	Manchu Hudson	8.8ab	5.4cd
Corsoy	6.5ab	4.1a-d	Beeson	9.8a-c	3.8a-d
Kanum	6.2ab	1.7a-c	Harosoy	7.9ab	0.8ab
Provar	6.5ab	2.9a-c	Black Eyebrow	9.9a-c	3.1a-c
Korean	10.1a-c	5.3b-d	Amsoy	14.3a-c	2.1a-c
Lindarin 63	11.2a-c	2.7a-c	Manchu Madison	15.1a-c	3.0a-c
Kanro	11.4a-c	0.7a	Hawkeye	17.7a-c	2.6a-c
Protana	11.5a-c	3.0a-c	Hawkeye 63	20.1bc	1.8a-c
Harosoy 63	11.9a-c	2.3a-c	Funman	24.6cd	10.1e
Mukden	13.3a-c	1.3a-c	Amsoy 71	32.6	1.9a-c
		Maturity Group III			
Guelph	0.1a	9.0d	Bavender Sp. B	11.5a-d	1.6ab
Little Wonder	4.3ab	0.6a	Lincoln	13.1a-d	1.5a
Cloud	5.0a-c	1.9ab	Chusei	13.8a-e	2.4ab
Jogun	5.2a-c	0.5a	Kanrich	14.4a-e	0.3a
Adams	5.5a-c	1.1a	SRF 350	14.9a-e	2.3ab
AK (Harrow)	5.6a-c	1.1a	Bavender Sp. B	15.0a-e	2.3ab
Ennis 1	6.9a-c	0.3a	Bavender Sp. C	15.0a-e	7.8cd
Kura	8.0a-d	1.0a	Mingo	15.7a-e	1.2a
Mandell	8.0a-d	0.6a	Adelphia	21.7a-e	1.9ab
Jogun (Ames)	8.5a-d	0.6a	Osaya	22.5a-e	5.1bc
Miller 67	8.8a-d	0.9a	Calland	25.2b-e	1.8ab
Ilsoy	8.8a-d	0.8a	Manchuria 20173	25.2b-e	2.2ab
Ford	8.8a-d	2.0ab	Manchu (Laf.)	26.8b-e	0.6a
Pennsoy	9.0a-d	1.4a	Manchuria 13177	28.4c-e	8.3d
Dunfield	9.6a-d	0.9a	Fugi	28.5c-e	2.2ab
Illington	9.0a-d	2.7ab	Manchu (Laf.) B	31.5de	3.2ab
Illini	10.5a-d	2.0ab	Columbia	36.5e	1.3a
Granger	10.8a-d	2.5ab	Mansoy	37.0e	3.6ab
Manchu	11.1a-d	2.4ab			
		Maturity Group IV			
SRF 425	6.1a	0.8a-e	AK (FC 30.761)	22.7a-j	0.2a-c
Funk Delicious	6.5ab	0.7a-d	Norredo	23.1a-j	1.0a-f
Boone	6.7ab	0.2ab	Hurrelbrink	23.2a-j	0.5a-c
Carlin	7.8a-c	0.5a-c	Patterson	24.9a-j	1.3a-f
Morse	8.1a-d	0.4ab	Kahala	26.3a-j	3.5d-i
Hahto (Michigan)	8.6a-e	1.6a-f	SRF 450	26.4a-j	1.9a-h

Table 1 (cont'd)

Cultivar	Undamaged pods	Damaged pods	Cultivar	Undamaged pods	Damaged pods
		Maturity Group IV (cont'd)			
Kingston	11.5a-e	1.4a-f	HP 963	27.7a-j	1.0a-f
Polysoy	12.2a-f	0.03a	Delmar	28.0a-j	4.6h-j
Harbinsoy	12.7a-f	1.3a-f	Bethel	29.0a-j	3.9f-i
Chief	13.3a-f	2.7a-i	Wye	30.0a-j	1.4a-f
Perry	14.2a-g	2.1a-h	Green and Black	31.3b-j	6.6j
Clark	14.8a-g	1.8a-h	Patoka	31.9c-j	4.5h-j
Cutler	15.1a-g	2.4a-i	Emperor	32.7c-j	3.0b-i
Higan	15.5a-g	1.7a-g	Hong Kong	32.8d-j	1.5a-f
Hokkaido	15.7a-g	1.7a-g	Macoupin	34.6d-j	2.7a-i
Fabulin	16.7a-g	1.8a-h	Kent	35.3e-j	3.7e-i
Kaikoo	17.0a-g	3.0b-i	D67-3297	36.1e-j	1.1a-f
Aoda	17.3a-g	1.0a-f	Cypress #1	37.1f-j	5.0ij
Ebony	18.0a-h	1.1a-f	Kingwa	37.2f-j	1.7a-g
Kailua	18.2a-h	1.5a-f	AK (Kansas)	38.4g-j	1.2a-f
Cutler 71	18.9a-h	2.0a-h	Columbus	42.1h-j	1.2a-f
Midwest	18.9a-i	2.5a-i	Custer	44.4ij	2.0a-h
Gibson	20.7a-i	0.8a-e	Oksoy	45.4ij	1.7a-g
Jefferson	20.8a-j	1.8a-h	Mokapu Summer	46.0j	2.6a-i
Clark 63	22.0a-j	3.9f-i	Peking	22.2a-j	0.6a-c
SRF 400	22.4a-j	3.4c-i			

Cultivars belonging to Maturity Groups 00 and 0 produced very few undamaged pods per plant because these cultivars suffered severe foliage and flower damage by H. zea. Significant differences were not observed for undamaged pods/plant for Maturity Groups 00 and 0 cultivars. However, 'Pando' and 'Ada' produced significantly more damaged pods than others in Maturity Group 00. Among Maturity Group I cultivars, 'OAC 211', 'A-100', 'Bombay', 'Kagon', 'Blackhawk', 'Elton', 'Chippewa', 'Hoosier' and 'Disoy' produced significantly more undamaged pods than others. However, 'Elton' produced the highest percentage of undamaged pods (89%) and 'Bombay' was a close second with 88%. 'Amsoy 71' and 'Funman' (Maturity Group II) produced 32.6 and 24.6 undamaged pods/plant respectively. These two cultivars have out-performed the others in their maturity group. However, Amsoy 71 and Funman produced 94.5% and 70.9% undamaged pods respectively. Amsoy 71 has certainly performed better than Funman. 'Mansoy' and 'Columbia' (Maturity Group III) produced 37.0 and 36.5 undamaged pods/plant respectively. However, the percentage of undamaged pods was 96.6 for Columbia and 91.1 for Mansoy.

Among Maturity Group IV cultivars 'Mokapu Summer' produced the highest number of undamaged pods/plant (46.0), followed closely by 'Oksoy' (45.4), 'Custer' (44.4), and 'Columbus' (42.1). The percentage of undamaged pods/plant was highest for Columbus. Soybean breeders, both public and private, may want to examine some of these entries more critically for developing resistant soybean cultivars.

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J. M. Joshi

2) Evaluation of soybean germplasm for resistance to corn earworm--II.*

During 1975, 145 additional soybean (Glycine max [L.] Merr.) Plant Introductions and cultivars belonging to Maturity Groups 00-IV were evaluated in the screen house for corn earworm (Heliothis zea Boddie) resistance. The experimental procedures were the same as described in the previous article except the number of corn earworm moths released in the screen house; 2,872 moths (2,244 released in 1974) were released from June 24 to September 19, 1975. Since a positive phenotypic correlation between the number of pods per plant and yield has been reported by many scientists (Anand and Torrie, 1963; Hanson and Weber, 1961; and Weatherspoon and Wentz, 1934), it is hoped that Plant Introductions

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and cultivars capable of producing more undamaged pods under heavy infestation will be both resistant and high yielding.

The mean numbers of undamaged and damaged pods per plant for each Plant Introduction and cultivar are reported below. The means not followed by the same letter are significantly different at the 0.05 probability level according to Duncan's Multiple Range Test.

Table 1

Mean undamaged and damaged pods for different soybean Plant Introductions and cultivars

Plant introduction or cultivar	Undamaged pods/plant	Damaged pods/plant	Plant introduction or cultivar	Undamaged pods/plant	Damaged pods/plant
		Maturity Group 00			
PI 194.627	1.4a	9.5a-d	PI 258.387	4.0a	14.8b-e
PI 189.937	1.5a	9.4a-d	PI 189.906	4.0a	14.7b-e
PI 194.647	1.5a	7.4ab	PI 194.644	4.3a	12.1b-e
PI 180.519	2.1a	12.3b-e	PI 180.516	4.8a	12.2b-e
PI 232.998	2.1a	11.7b-e	PI 258.386	4.9a	13.7b-e
PI 361.086	2.2a	8.3ab	PI 154.190	5.1a	7.0ab
PI 297.550	2.2a	19.0de	PI 358.321A	5.2ab	11.2b-e
PI 189.877	2.3a	7.8ab	PI 180.525	5.6ab	14.4b-e
PI 232.999	2.4a	11.2b-e	PI 180.507	5.6ab	8.1ab
PI 257.431	2.4a	10.0a-e	PI 180.508	5.8ab	15.3b-e
PI 194.624	2.9a	7.2ab	PI 154.197	6.6ab	19.5e
PI 189.880	2.9a	14.0b-e	PI 232.997	7.3ab	13.5b-e
PI 238.923	3.2a	18.0c-e	PI 154.193	10.8b	14.2b-e
PI 153.314	3.2a	12.0b-e	PI 297.503	13.1c	14.4b-e
PI 189.886	3.5a	7.2ab	Portage	13.9c	1.1a
PI 257.430	3.6a	14.6b-e			
		Maturity Group 0			
PI 261.475	0.7a	9.5a	PI 297.506	3.2a	15.2a
PI 290.114	1.1a	9.7a	PI 257.434	3.5a	10.1a
PI 297.516	1.5a	8.9a	PI 290.121	3.8a	7.1a
PI 291.312	1.5a	7.5a	PI 290.145	3.8a	13.5a
PI 290.131	1.8a	7.3a	PI 290.157	3.8a	13.3a
PI 290.122	2.0a	10.4a	PI 323.586C	4.1a	13.4a
PI 290.140	2.1a	10.9a	PI 290.118	4.2a	12.0a
PI 290.144	2.3a	9.7a	PI 290.115	4.4a	16.7a
PI 290.135	2.3a	7.7a	PI 347.549	4.5a	9.5a
PI 297.509	2.3a	8.6a	PI 257.436	5.3a	10.4a
PI 297.546	2.4a	8.9a	PI 290.123A	5.4a	14.0a
PI 297.547	2.7a	9.9a	PI 290.116A	5.8a	11.2a
PI 291.311A	2.8a	6.8a	PI 257.433	6.2a	11.2a
PI 290.141	2.8a	8.4a	PI 290.129B	8.3a	12.3a
PI 290.132	3.0a	11.2a	PI 297.512	3.1a	12.8a

Table 1 (cont'd)

Plant introduction or cultivar	Undamaged pods/plant	Damaged pods/plant	Plant introduction or cultivar	Undamaged pods/plant	Damaged pods/plant
		Maturity Group I			
PI 189.916	0.5a	8.7a	PI 297.505	1.4a-d	6.2a
PI 290.124	0.5a	7.6a	PI 290.134	1.4a-d	10.3a
PI 253.658A	0.8ab	1.9a	PI 253.652C	1.5a-e	6.3a
PI 184.042	0.9ab	5.3a	Wirth	2.2a-f	7.6a
PI 253.652D	0.9ab	2.6a	PI 361.095	2.6a-f	14.7a
PI 319.538	1.0a-c	4.9a	PI 291.322	2.8a-f	10.9a
PI 319.536C	1.0a-c	5.5a	PI 253.653D	3.0a-f	9.0a
PI 248.509A	1.1a-c	8.4a	PI 291.311B	3.5a-f	5.9a
PI 291.281	1.1a-c	6.0a	Dunn	3.7b-f	7.4a
PI 291.283	1.1a-c	4.4a	PI 291.304	3.8b-f	7.5a
PI 153.255	1.3a-d	5.7a	PI 266.806A	4.1c-f	10.2a
PI 253.653C	1.3a-d	6.4a	PI 361.092	4.3d-f	17.8a
PI 319.535B	1.3a-d	4.9a	PI 291.303A	4.5ef	7.9a
PI 297.548	1.3a-d	15.3a	PI 347.552B	5.0f	16.6a
		Maturity Group II			
PI 291.299	0.5a	2.7a	PI 266.806	1.9ab	5.0a
PI 291.282	0.7a	4.6a	PI 291.327	2.2ab	5.4a
PI 291.302B	0.7a	6.1a	PI 261.474	2.3ab	1.3a
PI 291.279	0.8a	2.3a	PI 85.021	2.9ab	2.3a
Kanro	0.8a	2.3a	PI 266.085B	3.0ab	5.1a
PI 291.306A	0.9a	6.1a	Yellow Marvel	3.6ab	2.6a
PI 317.334A	1.0ab	4.0a	PI 297.544	3.7ab	3.3a
Seneca	1.1ab	3.8a	PI 297.545	3.8ab	6.5a
PI 261.472	1.3ab	3.8a	PI 291.302A	4.2ab	2.3a
PI 340.007	1.5ab	1.2a	PI 86.089	4.4a-c	7.9a
PI 291.315	1.6ab	2.8a	PI 291.295	4.7a-c	11.1a
PI 266.085A	1.8ab	9.5a	Wells	10.6c	5.2a
PI 297.543	1.9ab	6.5a			
		Maturity Group III			
PI 86.153	0.3a	2.1ab	PI 261.466	2.0ab	0.8a
PI 84.976	0.3a	1.2a	Ennis I	2.4ab	2.2a-c
PI 86.075	0.4a	0.6a	PI 339.995	2.6ab	0.9a
PI 91.120-3	0.6a	1.0a	PI 86.073	3.1ab	3.3a-d
PI 253.660B	0.6a	3.1a-d	PI 273.483A	3.2ab	1.0a
PI 291.306B	0.9a	1.0a	PI 85.456	3.7ab	3.2a-d
PI 86.425	1.2a	0.4a	PI 86.071	4.8a-c	1.0a
PI 273.483A	1.3a	1.0a	PI 339.868E	5.9a-d	1.4a
PI 86.482	1.5a	2.2a-c	PI 253.661A	7.3b-e	2.2a-c
PI 261.467	1.7ab	3.0a-d	Wayne	9.7c-e	6.1de
Wolverine	1.8ab	1.8ab			

Table 1 (cont'd)

Plant introduction or cultivar	Undamaged pods/plant	Damaged pods/plant	Plant introduction or cultivar	Undamaged pods/plant	Damaged pods/plant
		Maturity Group IV			
T141	2.4a	0.3a	D66.5566	17.2a-e	0.3a
T31	3.5ab	2.6a	T145	19.5a-e	0.2a
Sanga	6.9a-d	1.8a	PI 86.740	27.9b-f	0.6a
T207	7.1a-d	1.5a	PI 86.876	31.0c-g	2.1a
T240	10.1a-e	1.8a	Gibson	16.0a-e	1.0a

Soybean cultivar 'Portage' in Maturity Group 00 produced the highest number of undamaged pods and only 1.1 damaged pods/plant. Among all the Plant Introductions and cultivars tested in Maturity Group 00, Portage has outperformed the rest. Significant differences were not observed in any tested Plant Introduction or cultivar in Maturity Group 0 for either undamaged or damaged pods. The number of undamaged pods produced by the Plant Introductions or cultivars in Maturity Groups I, II, and III was very low; the highest number of undamaged pods (10.6) was produced by 'Wells'. PI 86.876 in Maturity Group IV produced the highest number of undamaged pods (31.0), followed closely by PI 86.740, which produced 27.9 undamaged pods/plant. The percentage of undamaged pods was higher, however, for PI 86.740 (97.9%) than PI 86.876 (93.3%). These data indicate that cultivar Portage and Plant Introductions PI 86.740 and PI 86.876 resist corn earworm damage better than other tested cultivars or Plant Introductions.

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J. M. Joshi

3) Effect of soybean plant age on the expression of antibiosis to corn earworm.

It is expected that soybean (Glycine max [L.] Merr.) cultivars resistant to various insect pests shall play an important role in integrated pest management programs. Certain soybean cultivars have been shown to possess resistance to Mexican bean beetle (Epilachna varivestis Mulsant) (Van Duyn et al., 1971, 1972), bean leaf beetle (Cerotoma trifurcata Foster), striped blister beetle (Eplicanta vittata Fabricius) (Clark et al., 1972) and corn earworm (Heliothis zea Boddie) for leaf feeding (Beland and Hatchett, 1976; Joshi and Wutoh, 1976; Joshi, 1977; Hatchett et al., 1976). It has been suggested that 2 to 3 weeks age difference has considerable effect on the expression of antibiosis to corn earworm as expressed by low larval weight and higher larval mortality in cases of resistant genotypes. However, the behavior of the commercial cultivars was not consistent and the larval weights were generally higher (Hatchett et al., 1976; and Beland and Hatchett, 1976). The present investigation was undertaken to study the effect of plant age on the expression of antibiosis to corn earworm.

Materials and methods: Three Plant Introductions and three cultivars (PI 227.687, PI 229.358, ED 73.371, 'Shore', 'Wye' and 'Davis') were planted in the greenhouse on April 2, 1977. Promix was used as a seed bed material and the pH was adjusted by mixing 5 pounds of dolomite lime/cubic yard. Soybean cultivar Davis (Hatchett et al., 1976) and synthetic diet (supplied by Bio-Serv, Frenchtown, NJ) were used as checks. Two separate tests were conducted. First test of antibiosis was started on May 11, 1977 when most of the plants were in the 5th trifoliolate stage, but cultivars Shore and Wye were in flowering stage. Second test was started on June 20, 1977. Plants in Test 2 were 40 days older than in Test 1. PI 229.358, PI 227.687 and Davis were the only ones included in Test 2. Others could not be used due to the

lack of fresh vegetative growth. Synthetic diet treatment was again included as check in Test 2. The mean temperature was 24.2°C (range 21-27°C) during Test 1 and 25.6°C (range 23-28°C) during Test 2. Three newly hatched larvae (< 24 hr old) were placed in 75.0 ml plastic lidded cups with moistened disc of paper toweling along with the excised leaflet of the uppermost fully expanded trifoliolate. The paper discs were moistened to help maintain high humidity for larvae and to retard water loss from the leaflets. Each treatment had 30 cups per treatment. After 72 hr, larvae were thinned to 1 per cup. The larvae were weighed on 16th day and pupae on 5th day after pupation in both tests. The duration of larval period, pupation period, larval mortality and total mortality were also recorded. Other techniques of feeding and rearing were the same as reported in the earlier publications (Joshi and Wutoh, 1976; Joshi, 1977).

Results and discussion: The effect of different feeding treatments on the growth and development of H. zea is given in Table 1. In Test 1, which represented leaf feeding from younger plants, larvae gained least weight on Shore (216 mg), although there was no significant difference in larval weight among Shore, ED 73.371, and PI 227.687. As expected, maximum larval weight was gained on synthetic diet (600 mg). However, no significant difference was observed in the larval weight for Wye and Davis (susceptible check). The larval weight on Davis was also not significantly different from PI 229.358 (resistant check). Larvae feeding on Shore and ED 73.371 passed through extended larval stage and spent 24.5 and 23.5 days respectively in larval stage. On the contrary, the larval duration was only 18.9 days on synthetic diet. The larval stage on Wye and Davis was 19.9 and 21.0 days, respectively, and were not significantly different from each other. The duration of the pupal stage was not influenced by any Plant Introduction or cultivar. However, the larvae raised on synthetic diet had extended pupal stage. The total mortality was very low on PI 229.358. The other resistant genotypes, however, showed higher mortality as compared to synthetic diet, Davis and Wye. The highest mortality was observed for ED 73.371 (43.3%), followed by PI 227.687 and Shore (30%).

Test 2 was started on June 20, 1977 on the same plants. The plants in Test 2 were more advanced in age, i.e., 40 days older than in Test 1. The data in Test 2 (Table 1) clearly indicates the H. zea larvae gained less weight when raised on the foliage of older plants. The larvae gained less

weight on PI 229.358, PI 227.687 and Davis. The total mortality increased on the 2 Plant Introductions (PI 229.358 and PI 227.687) and decreased on Davis. These results are consistent with earlier studies (Hatchett et al., 1976; and Beland and Hatchett, 1976). The total mortality on PI 227.687 was 80% in Test 2 and only 30% in Test 1. Total H. zea mortality on different genotypes in this study was very low except for PI 228.687 in Test 2 (80%). Much higher mortalities have been reported by other investigators (Hatchett et al., 1976; and Beland and Hatchett, 1976). It is not clear whether the difference in total mortality is due to environmental conditions or variability in the vigor of the H. zea larvae of different females or both.

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4) Observations on a new important pest of soybeans.

In 1976, the alydid, Alydus pilosulus (H.-S.), was first recorded in small numbers on the research plots at Princess Anne, MD. But in 1977, it was observed in pest proportions and also a corid, Leptoglossus oppositus (Say), was recorded for the first time. Though the stink bugs were not observed to

Table 1

Treatment[+]	Larval weight[++] (mg)	Larvae pupated (#)	$\bar{X}$ days to pupation	Pupal weight[+++] (mg)	$\bar{X}$ days in pupation	Larval mortality (%)	Total mortality (%)
			Test 1				
Synthetic diet	600a*	29	18.9d*	432a*	15.4a*	3.3	6.7
Wye	470b	27	19.9cd	273bc	13.7b	10.0	10.0
Davis	402b-d	26	21.0c	288b	14.0b	13.3	20.0
PI 229.358	369cd	29	22.7b	278b	13.9b	3.3	6.7
PI 227.687	291de	24	22.6b	262b-d	14.1b	20.0	30.0
ED 73.371	231e	20	23.5ab	275bc	13.7b	33.3	43.3
Shore	216e	22	24.5a	235d	13.0b	26.7	30.0
			Test 2[++++]				
Synthetic diet	490a	28	14.7d	410a	10.3a	6.7	10.0
Davis	380b	28	19.5c	230b	9.9a	6.7	10.0
PI 229.358	250c	25	22.7b	210b	9.6a	16.7	20.0
PI 227.687	180d	14	23.0a	160c	9.3a	53.3	80.0

*Means not followed by the same letter were significantly different at the 0.05 probability level according to Duncan's Multiple Range Test.

[+]30 larvae/treatment.

[++]Mean weight of larvae on 16th day.

[+++]Mean weight of pupae on 5th day after pupation.

[++++]Plants 40 days older than in Test 1.

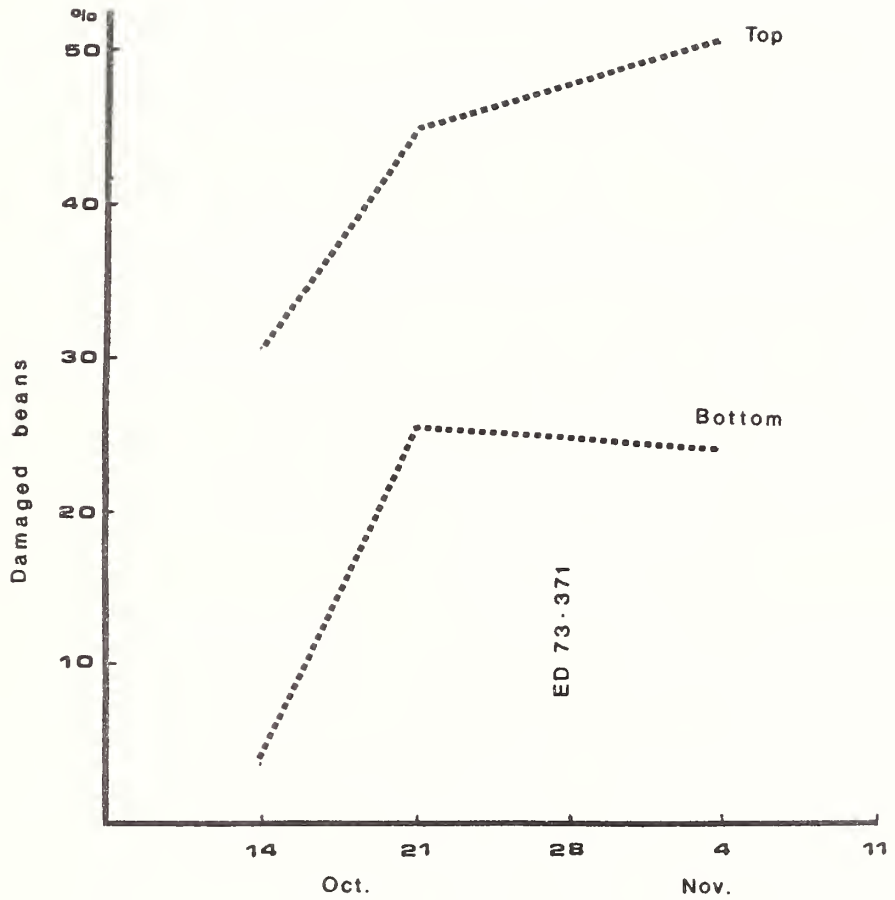

Fig. 1. Mean damaged beans from top and bottom of soybean plants.

be more numerous than in the previous years, the total damage from feeding by all the heteroptera was assessed by obtaining five yellow or green pods from the uppermost portion of the plant and five pods from the lowest part of the same plant; ten plants were sampled from a 9'x20' plot. The pods were shelled by hand and the beans examined for damage. The results are presented in Fig. 1.

Yeargan (1977) has shown that when four green stink bugs (A. hilare) were present per 0.3 m of row, the damaged pods were 36.5%. Our overall means, excluding the sample from ED 73.371, are 42.1% for the top and 17.9% for the bottom. No increase in damage at the bottom of the plant, in the last sample, could be due to the earlier maturity of these pods in a plant.

Acknowledgement: Facilities provided by Dr. J. M. Joshi, Director, Soybean Research Institute, University of Maryland, Eastern Shore, Princess Anne, MD, are gratefully acknowledged.

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1) Correlated response of certain plant traits with seed yield in soybeans.

Soybean (Glycine max [L.] Merr.) breeders are constantly searching for plant traits that are associated with high seed yield. Breeders have made use of correlated responses in the selection procedures for high yield and disease resistance, high protein and low oil content, and days to maturity and seed yield. Several plant traits such as lodging, plant height, shattering, maturity, etc. must be simultaneously taken into consideration in the selection process. It has been observed that plant height, late maturity and susceptibility to lodging are positively correlated with seed yield (Anand and Torrie, 1963; and Kwon and Torrie, 1964). Plant traits such as short stature and resistance to lodging have been reported to have association with seed yield (Byth et al., 1969). Low seed yield has been associated with indeterminate growth and glabrousness (Hartwig and Edwards, 1970). So far the study

of correlated responses has not provided useful selection criteria for increasing seed yield and one of the reasons for insufficient progress in this direction may be that the traits studied so far are not more closely related to physiological processes associated with seed yield.

The present investigation was undertaken to determine the extent of association between seed yield and certain plant traits such as unthreshed plant weight, non-seed dry matter weight, number of pods, days from flowering to maturity, number of branches, undeveloped ovules, plant height and number of seeds per plant.

Materials and methods: Ten soybean cultivars were selected on the basis of their diversity in maturity, plant height and growth habit for this study. The seedlings grown in the greenhouse were randomly planted in the field and spaced 91 cm apart in 71 cm rows during 1971 at the Agronomy Farm of the Ohio State University, Columbus, Ohio. The number of single plant replications were: 'Aoda', 12; 'Cayuga', 9; 'Giant Green', 8; 'Habaro', 20; 'Hakote', 9; 'Henry', 46; 'Kent', 39; 'Kura', 13; 'Manchuria', 7; and 'Wayne', 45. Each plant was harvested at maturity at ground level, bagged separately in a cloth bag and analyzed. The unthreshed weight of the plant included air-dry weight of stem, branches, pods and seeds; non-seed dry weight was calculated by subtracting seed yield from its weight. The step-wise multiple regression method was used to calculate the relative importance of traits associated with seed yield.

Results and discussion: The data on ten soybean cultivars for certain plant traits have been given in Table 1. Plant traits which contribute most in improving seed yield have been listed in order of their importance in Tables 2 and 3. Unthreshed weight and non-seed dry matter weight when considered together in the step-wise multiple regression analysis, along with other traits, gave an r value of 1, after the selection of unthreshed weight and non-seed dry matter weight. Other traits which also had appreciable influence on yield could not be considered in this way. Therefore, it was desirable to evaluate these traits in two sets of data: one set with non-seed dry matter weight and the rest of the traits (Table 2), and the other set of data with unthreshed weight and the rest of the traits (Table 3). It is clear from Table 2 that substantial improvement in r values was made by non-seed dry matter weight. Variability of 98.38% in yield is due to non-seed dry matter weight. Number of pods/plant is the second important trait which, along with

Table 1

Values/plant for certain traits in 10 soybean cultivars

Cultivar	Unthreshed wt. (g)	Non-seed dry matter wt. (g)	Flowering to maturity (Days)	Pods (#)	Branches (#)	Undeveloped ovules (#)	Height (cm)	Seeds (#)	Seed yield (g)
Aoda	47.8	20.6	99.7	68.5	15.6	36.8	32.3	80.4	27.2
Cayuga	23.5	9.3	59.2	46.3	5.9	15.3	33.1	102.3	14.2
Giant Green	22.9	9.8	67.8	39.3	6.0	15.8	25.4	59.4	13.1
Habaro	32.8	13.1	75.2	66.0	7.7	17.1	28.9	114.4	19.7
Hakote	31.9	12.8	86.4	50.6	10.3	16.7	25.6	76.3	19.1
Henry	49.4	21.4	83.8	81.3	11.8	32.4	43.6	171.5	28.0
Kent	99.2	40.2	117.7	150.4	15.5	83.8	59.6	318.1	59.0
Kura	43.1	18.4	105.6	56.9	11.5	14.9	20.6	86.8	24.7
Manchuria	24.0	9.1	68.7	52.0	5.6	12.0	20.4	89.3	14.9
Wayne	78.4	30.8	97.1	132.1	10.5	57.0	52.7	280.5	47.6

non-seed dry matter weight, improves the r up to 0.9977. These two traits accounted for 99.53% of the variability in yield.

Table 2

Step-wise multiple regression of certain traits with seed yield (unthreshed weight excluded)

Dependent variable	r	r^2	% increase in RSQ	Standard error	F value
Non-seed dry matter weight	0.9919	0.9838	98.38	2.0515	486.77
Pods	0.9977	0.9953	1.15	1.1790	17.22
Days from flowering to maturity	0.9983	0.9967	0.14	1.0757	2.41
Branches	0.9987	0.9975	0.08	1.0229	1.64
Undeveloped ovules	0.9993	0.9986	0.11	0.8590	3.10
Height	0.9998	0.9995	0.09	0.5630	6.31
Seeds	0.9998	0.9996	0.01	0.6693	0.12

Table 3

Step-wise multiple regression of certain plant traits with seed yield (non-seed dry matter weight excluded)

Dependent variable	r	r^2	% increase in RSQ	Standard error	F value
Unthreshed weight	0.9987	0.9974	99.74	0.8151	3126.10
Branches	0.9995	0.9990	0.16	0.5525	10.41
Pods	0.9996	0.9991	0.01	0.5575	0.88
Height	0.9997	0.9993	0.02	0.5528	1.82
Undeveloped ovules	0.9997	0.9994	0.01	0.5550	0.44
Days from flowering to maturity	0.9998	0.9995	0.01	0.5744	0.74
Seeds	0.9998	0.9995	0.00	0.7001	0.02

The r value between unthreshed weight and seed yield was 0.999 (Table 3). Unthreshed weight and number of branches together improved the r value to 0.9995 and accounted for 99.90% of the variability in seed yield. It was further noted that the standard error of the estimate was lowest at this point and thereafter it started to increase. This was an indication that no appreciable gain in seed yield could be made by considering other traits.

These data suggest that selection based on non-seed dry matter weight or unthreshed weight should be helpful in improving soybean yield. Since it is easier to record unthreshed weight than non-seed dry matter weight and in view of its higher r value with seed yield, more emphasis should be placed on unthreshed weight in the selection process.

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1) Screening soybean seed for lectin content.*

Soybeans [Glycine max (L.) Merr.] contain at least four glycoproteins that are capable of clumping red blood cells (Catsimpoolas and Meyer, 1969;

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Lis et al., 1966; Rackis et al., 1959; Stead et al., 1966). These glycoproteins are called lectins. The lectin content in defatted soybean meal is about 3% (Liener and Rose, 1953). The major lectin in soybean seed, termed soybean lectin (SBL), has a molecular weight of 120,000 and specificity for D-galactose and N-acetyl-D-galactosamine (Bhuvaneswari et al., 1977; Lotan et al., 1974). We report the results of an experiment to determine whether SBL-free lines exist within the soybean germplasm.

Seeds of 102 soybean lines were ground and defatted with petroleum ether. An aliquot of each meal (1 to 2 g) was extracted for 2 hr with phosphate-buffered saline containing radioisotope-labeled SBL of known specific activity (Lotan et al., 1975). Each extract was clarified and subjected to affinity chromatography using a Sepharose affinity adsorbent derivatized with N-acylgalactosamine as described by Pueppke et al. (in press). Each column eluant containing SBL was dialyzed and its specific activity determined by liquid scintillation spectrometry and its protein content determined by the method of Lowry et al. (1951).

For 97 lines, the range in amount of SBL was from 2.5 to 12.2 mg SBL/g defatted meal (Table 1). The range in SBL content in soybean protein was from 0.6 to 5.0%. The remaining 5 lines ('Columbia', 'Norredo', 'Sooty', T 102 and 'Wilson-5') lacked any detectable SBL.

Several additional tests were conducted to determine if even trace amounts of lectin could be detected in the seeds of the 5 soybean lines lacking SBL. Hemagglutination, binding to cells of certain rhizobia strains and polyacrylamide gel electrophoresis experiments failed to detect the presence of SBL in the seed of the 5 soybean lines.

At present, investigations are being conducted to determine the mode of inheritance of SBL in soybean seed.

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Table 1

Lectin content in soybean seed

Line	SBL (mg/g meal)	Protein (mg/g meal)	SBL in protein (%)	Line	SBL (mg/g meal)	Protein (mg/g meal)	SBL in protein (%)
Ada	9.1	310	2.9	Fabulin	5.4	312	1.7
Adelphia	2.6	287	0.9	Fiskeby V	5.5	259	2.1
A.K.	8.0	194	4.1	Flambeau	6.6	342	1.9
Amsoy	7.1	366	1.9	Fuji	4.6	214	2.1
Anoka	8.6	355	2.4	Funk Delicious	4.7	286	1.6
Aoda	3.1	253	1.2	Giant Green	3.5	248	1.4
Bansei	5.5	298	1.8	Gibson	5.2	356	1.5
Bavender	4.5	330	1.4	Granger	7.4	202	3.7
Beeson	7.8	308	2.5	Green and Black	5.4	266	2.0
Blackhawk	6.1	332	1.8	Harbinsoy	4.1	326	1.2
Bombay	4.6	289	1.6	Harcor	12.2	244	5.0
Capital	6.6	354	1.9	Harmon	10.6	358	3.0
Cayuga	4.5	231	1.9	Harosoy 63	5.8	356	1.6
Chippewa	5.7	333	1.7	Harwood	6.3	370	1.7
Chusei	5.8	276	2.1	Higan	4.9	235	2.1
Clay	5.5	370	1.5	Hokkaido	2.8	334	0.8
Cloud	5.0	359	1.4	Hoosier	5.3	352	1.5
Columbia	0.0	254	---	Illini	7.0	270	2.6
Corsoy	6.4	259	2.5	Imperial	4.9	221	2.2
Cutler	6.6	254	2.6	Jogun	4.1	425	1.0
Cypress #1	3.6	390	0.9	Kabott	4.9	395	1.2
Dunn	8.0	391	2.0	Kagan	4.6	249	1.8
Early White Eyebrow	5.4	251	2.2	Kanro	2.6	412	0.6
Ennis I	8.8	294	3.0	Kent	7.8	297	2.6

Table 1 (cont'd)

Line	SBL (mg/g meal)	Protein (mg/g meal)	SBL in protein (%)
Kim	2.7	207	1.3
Kura	4.5	342	1.3
Linman	8.9	292	3.0
Little Wonder	4.7	278	1.7
Madison	5.6	296	1.9
Magna	4.6	250	1.8
Manchu	4.7	254	1.8
Manchuria	3.8	376	1.0
Mandarin	6.0	359	1.7
Manitoba Brown	4.0	222	1.8
Medium Brown	6.0	298	2.0
Merit	9.2	355	2.6
Mingo	6.7	277	2.4
Mokapu Summer	6.3	376	1.7
Morse	6.6	272	2.4
Norman	5.4	357	1.5
Norredo	0.0	179	---
Ogemaw	6.0	275	2.2
Oksoy	4.4	330	1.3
Ontario	10.2	384	2.6
Ottawa	3.8	299	1.3
Pando	4.9	277	1.8
Peking	4.2	237	1.8
Perry	2.5	371	0.7
Portage	6.6	264	2.5
Portugal	3.8	362	1.0
Protana	7.6	280	2.7
Provar	4.0	388	1.0
Rampage	8.1	259	3.1
Ross	9.0	335	2.7
Sato-3	3.9	241	1.6
Scott	5.7	354	1.6
Seedmakers	4.9	361	1.4
Sioux	4.0	225	1.8
Sooty	0.0	251	---
Soysota	7.8	225	3.5
SRF 400	10.3	280	3.7
Steele	3.9	368	1.0
Swift	5.5	320	1.7
T102	0.0	218	---
Tortoise Egg	4.6	304	1.5
Vansoy	7.7	324	2.4
Viking	3.9	252	1.5
Waseda	2.5	378	0.7
Wea	6.8	429	1.6
Wilson	6.9	255	2.7
Wilson 5	0.0	327	---
Wilson 5B	6.6	347	1.9
Wilson 6	7.6	382	2.0
Wing Jet	7.3	272	2.7
Wisconsin Black	7.4	246	3.0
Wolverine	3.7	423	0.9
Wye	6.8	290	2.3
Yellow Marvel	4.9	231	2.1

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1) Hilum color as a genetic marker in soybean crosses.

Artificial crossing of judiciously selected parents is a primary component of any soybean breeding program. Once hand-pollinations are made, however, it is crucial that actual crosses be distinguished from inadvertent female parent selfs prior to the planting of the F_2 seed, since considerable labor and land resources would be wasted on putative F_2 seed progenies that are later identified as the selfed progeny of the female parent used in the cross.

While emasculation of the flowers of the female parent minimizes the occurrence of accidental selfs, removal of the anthers adds considerable time to each hand pollination (resulting in fewer crosses made) and inexperienced student or part-time workers often injure the female parts of the flower

(resulting in a low success rate). Simple genetic markers, such as flower, pubescence and pod color can be and are used by soybean breeders in lieu of emasculation to distinguish F_1 crosses from selfs. However, in many cases the two chosen parents do not have the contrasting phenotypes to allow use of these simple monogenic markers.

In the soybean breeding program at the University of Nebraska, we have found that hilum color serves as a very useful genetic marker in most of the crosses we make each year. In most of the adapted cultivars and strains used for crossing by soybean breeders, hilum color is determined by four gene loci, namely, $\underline{I}/\underline{i}^{i}$, $\underline{R}/\underline{r}$, $\underline{T}/\underline{t}$, and $\underline{W}_1/\underline{w}_1$ (Bhatt and Torrie, 1968; Bernard and Weiss, 1973). These four gene pairs interact to produce the six hilum color phenotypes shown in Table 1. Note that two of these gene pairs also influence flower ($\underline{W}_1/\underline{w}_1$) and pubescence ($\underline{T}/\underline{t}$) color. The hilum color of F_1 seed coats (surrounding F_2 seed embryos) arising from the various crosses of parental hilum colors is shown in Table 2.

On the basis of the simple nonlinked inheritance and the known phenotypic interactions of the four gene pairs, we have constructed a simple flow chart (Figure 1) indicating the direction (arrows in chart) of pollen transfer between two parents differing in hilum color, such that the F_1 cross can be distinguished from a female parent self on the basis of the hilum color of the F_2 seed progeny. This chart is used when we are deciding which of two selected parents is to be the male. For example, if a cross between a parent with a grey hilum and a parent with a yellow hilum (or any other hilum color in this case) was desired, the chart indicates that the former should be the male parent. Note that in some instances the cross between two contrasting hilum colors can be made in either direction. This is because the F_1 hilum color differs from either parental hilum color (e.g., Y x Bl or Bl x Y results in a G F_1).

The use of hilum color as a genetic marker for soybean crosses has several advantages. First, there are six different hilum color phenotypes (rather than two in the case of a simple monogenic marker) and if flower and pubescence color are scored as well, there are 14 phenotypes available. This increases the probability that any two parents chosen for crossing would differ in phenotype. Consequently, these genetic markers can be used in nearly all crosses, particularly in view of the rather common occurrence of both alleles of the four loci in soybean cultivars and breeding strains. Second, the decision as to which way to make a cross can be made by observing the seed

Table 1

Hilum, pubescence and flower color phenotypes of the 16 genotypes arising from the four gene pairs $\underline{I}/\underline{i}^{i}$, $\underline{R}/\underline{r}$, $\underline{T}/\underline{t}$ and $\underline{W}_1/\underline{w}_1$

Genotype	Phenotype*			
	Hilum color		Pubescence color	Flower color
	With $\underline{i}^{i}$	With $\underline{I}$		
RTW_1	Bl	G	T	P
RTw_1	Bl	G	T	W
RtW_1	Ib	G	G	P
Rtw_1	Bf	Y	G	W
rTW_1	Br	Y	T	P
rTw_1	Br	Y	T	W
rtW_1	Bf	Y	G	P
rtw_1	Bf	Y	G	W

*Abbreviations used include Grey, Yellow, Black, Imperfect black, Brown, Buff, Tawny, Purple and White.

Table 2

Hilum color of F_1 seed coats derived from all possible crosses of parental hilum colors

♀ \ ♂	G	Y	Bl	Ib	Br	Bf
G	G	G	G	G	G	G
Y	G	G/Y*	G	G	G/Y*	G/Y*
Bl	G	G	Bl	Bl	Bl	Bl
Ib	G	G	Bl	Bl	Bl	Ib
Br	G	G/Y*	Bl	Bl	Br	Bl/Br*
Bf	G	G/Y*	Bl	Bl	Bl/Br*	Ib/Bf*

*Crosses (and reciprocals) involving a Y or Bf parent with a Y, Br or Bf parent will result in the F_1 hilum color to the left of the slash if the Y or Bf parent has an RR genotype and if the Y, Br or Bf parent has a TT and/or a $\underline{W}_1\underline{W}_1$ genotype.

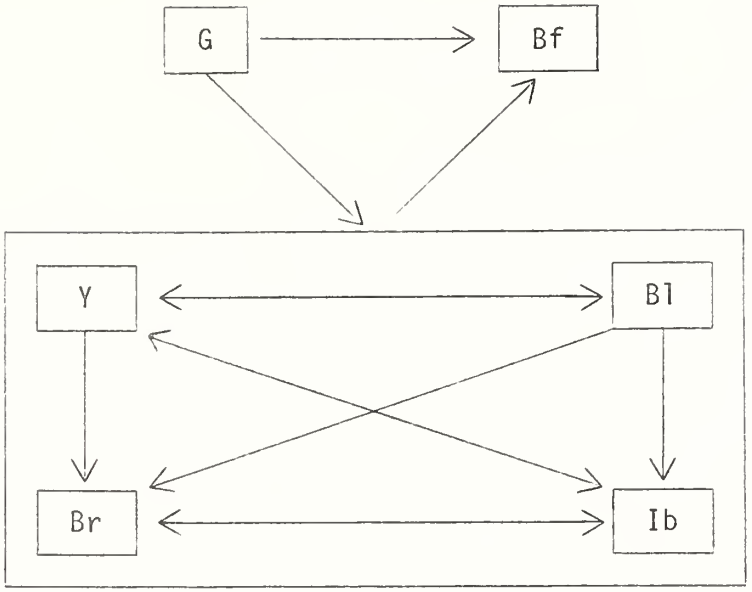

Fig. 1. A chart illustrating the direction (arrows) of pollen transfer between two parents of different hilum color phenotypes if the F_1 is to be distinguished from a self on the basis of hilum color.

phenotype, which in many cases may be the only descriptive trait known for one or both parental strains at the time. Third, two of the genes controlling hilum color also control flower and pubescence color which are already widely used genetic markers for crosses. Finally, no additional generation is required when hilum color is used since the seed borne on putative F_1 plants can be examined for hilum color at maturity prior to harvest. The information in Table 2 can then be used as the criterion for deciding whether the putative F_2 seed arose from a cross or accidental self and, if the latter, the plant can be discarded without harvesting.

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1) Soybean research and breeding in Poland.

Soybean has been subjected to research and breeding in Poland for dozens of years. Despite development of native varieties, soybean has not yet been cultivated on a large scale. The evergrowing demand for commercial protein intensified interest in this plant. In 1972, the Institute of Genetics and Plant Breeding, Academy of Agriculture, Poznan worked out a long-term research program on soybean genetics and breeding under climatic conditions of Poland, particularly for the region of Greatpoland [latitude 51°30' — 53°].

The program involves genetic, breeding and physiological aspects besides cultivation problems to some extent. The work is primarily aimed at establishing genotypes with growing period not longer than 130-135 days and also of profitable characters for agricultural practice.

Considering the recent progress in soybean genetics and breeding which had basically changed the geographical regions of soybean cultivation extending them to the north [to 58° latitude, Sweden], it was decided that efforts first be made on setting a germplasm collection of varieties and strains arranged in Maturity Groups 00-IV. Seed samples were collected from various countries, the majority from the U.S.A. [Urbana-Champaign, IL], next from Canada, Sweden, the U.S.S.R. and Japan. The total number of entries (2,412) included 275 varieties and 2,137 genetic lines. As a result of four-year field experiments, 580 forms were selected which matured in the open. Of these, 126 forms had vegetation period ranging from 125 to 140 days. The evaluation test was very severe due to extremely varying and unfavorable weather conditions prevailing during the experiment. Conspicuous differences were found between the classification to maturity groups according to Dr. Bernard [U.S. Regional Soybean Laboratory, Urbana, IL] and the growing period in our experimental conditions (discrepancies approximated 4-6 weeks). The initial evaluation (based on single plants) revealed that some of the ripening forms could be directly selected while the carriers of valuable genes (viz. yielding capacity and morphotype) could be used as components in crosses. In 1977, 2,500 plants were selected for developing lines, their propagation and yield evaluation.

Since 1976, an extensive program of crossing has been implemented. It was designed to obtain recombinants and at the same time to make observations on inheritance and hereditary processes of various traits. The crossing pattern followed is based on one very early parental plant and the other carrier of advantageous traits (i.e., yielding capacity, morphotype, resistance to diseases, etc.). The F_1 and F_2 hybrids are currently under further evaluation. The program on hereditary traits of soybean with regard to yield and mechanical harvesting in our environment has been continuously extended. Also, the program includes experiments on heritability of traits at different plant spacing.

Evaluation of collection forms is paralleled with work on extension of genetic variation through inducing mutations. Of the collection, 20 varieties with different genetic and developmental characteristics (that matured under Polish environmental conditions) were selected and later subjected to gamma radiation and chemicals (MMS, PMS, EES, EMS, NEU, NMU, ES and $NaNO_3$) separately and in combinations. Analysis of germination, emergence, teratological changes, growth and development, survival and reproduction in M_1 generation revealed specific response of the analyzed varieties to the applied mutagens (Jaranowski and Skorupska, 1977). In M_2, work was started on isolation of mutations primarily from the viewpoint of advantageous characters for breeding. Some 50 mutant lines in M_4 generation are currently under evaluation. Those with the advantageous "harvesting criterion" trait seem to be promising.

Observation on biology of flowering of the collected forms showed the process not to be sufficiently known in our climatic conditions. There was a lack of comprehensive information regarding primarily morphogenesis of flowers, process of flowering and the overall effectiveness of flowering. Hence, in 1977 a detailed study was initiated on the biology of flowering. The study covers 120 forms carefully selected from the collection. The methods employed are following: cyto-embryological, anatomical, morphological, developmental, quantitative determination of effectiveness of flowering, etc. The 1977 results, particularly the range of variation of the analyzed characteristics, prove expediency of the studies.

Since 1976, field experiments with 25 selected forms have been carried out to set up an effective selection index primarily with respect to the yielding capacity. The obtained results (characteristics of 17 traits) will be elaborated using the pathway coefficient. The initial results from two-year experiments are very interesting.

In 1976, a series of experiments was started on tolerance of varieties to sowing in early spring. The two-year results indicate the response to early sowing to be specific (beginning from the date of sowing pea). The evidence showed that the early date of sowing did not induce early flowering or maturity. However, optimum sowing date was possible to establish. This is a significant finding, since the problem lies in using ground water stored in winter. In our conditions where water-deficient periods appear continually in late spring and early summer, it is of vital importance for emergence and initiation of development of plants. The three-year series of results are interesting from the biological as well as from the practical viewpoint and will be elaborated by the end of 1978.

The kind assistance of Dr. T. Hymowitz and Dr. H. Hadley provided grounds for one-year fellowship training of Dr. H. Skorupska of our Institute in 1976-77. Dr. Skorupska was given an opportunity to learn the recent methods used in genetic research as well as to participate in studies on heritability of certain proteins in soybean seeds, origin and domestication of soybean, use of male sterile lines in crosses and induction of cytoplasmic male-sterility. Results of these studies were partly published (Skorupska and Hymowitz, 1977) and are being partly prepared for publication. The studies described above have been incorporated into our research program and will serve to help understand the basic genetic processes in soybean and such information can be later effectively utilized in breeding work.

Sincere thanks are due to Drs. R. Bernard (Urbana, IL) and R. Palmer (Ames, IA) for their thought-providing discussions on methodological aspects. The exchange of plant material (particularly of ms lines) is also greatly appreciated.

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1) Yield components and development of several soybean varieties under various climatic conditions in Switzerland.

Our work on soybeans is intended to provide information bearing on the following questions: (1) Can soybeans be cultivated in our country at expenses tolerable to agriculture; and (2) if not, what must be undertaken in order to achieve this objective?

We would like to insert the soybean as a suitable leguminous plant in our crop rotation (in 1975, 61% of the fields in Switzerland were cultivated with small grains and 17% with corn) and to benefit from this rich source of protein (as animal and perhaps as human nutrition). The study of growth, development and morphological yield formation and of the effects of fructification are important in determining the agricultural potential of the soybean in Switzerland.

Our investigations with different varieties (Maturity Group 000-II) concerning yield formation and the development of several soybean varieties under various climatic conditions have shown that the economic returns, particularly in northern Switzerland and to a lesser degree in western Switzerland, are unprofitable. The plants form a good vegetative structure (stems, branches, leaves and nodes) under all the climatic conditions investigated. Vegetative development itself requires a rather high temperature sum until anthesis. Anthesis takes place only in the middle of July because of the cooler temperatures in north Switzerland; therefore only about 60-80 days and a relatively low temperature sum remain available for pod and seed formation and for the filling phase of the seeds.

The test of yield components under various climatic conditions has indicated large differences between cultivation sites. The yield potential, as determined by the number of flowers per plant, was available under all climatic conditions. For example, plants growing at the location having cooler temperatures demonstrated a clearly higher percentage of aborted flowers and pods. The complex questions concerning floral and pod abortion must be studied further, although investigations are considerably difficult due to the small size of the flowers.

The improvement of yield components of the soybean is desirable. Our intention was to analyze the most important yield components for use in a possible subsequent breeding program. Our results have indicated that an increase in thousand seeds weight leads to an increase in yield, while the other components are presumed to remain constant. Next to thousand seeds weight, which is relatively strongly influenced by genetics, early maturity must certainly be taken into consideration. The following factors must be studied within the scope of a breeding program: inheritance of yield components and particularly inheritance of the thousand seeds weight, as well as inheritance of days to anthesis and to maturity.

The varieties 'Fiskeby V' (Sweden, Maturity Group 000) and 0-52-903 (Ottawa Research Station, Maturity Group 000) reached full maturity under all the climatic conditions studied. Both varieties, however, showed a small economic yield. On the other hand, other varieties (e.g., 'Dunn' and 'Anoka', both from the U.S. and of Maturity Group I) indicated a high yield potential (higher number of pods per plant combined with a large number of seeds and a relatively high thousand seeds weight), under optimum growth conditions. The prerequisites for the cultivation of soybean under our climatic conditions do exist, inasmuch as it will be possible by means of actual breeding, to optimally combine the breeding objectives of early maturity, yield ability and reliability of yield.

The field trial experiments and especially those in the plant growth chambers, have indicated the great importance of cold tolerance of the soybean in Switzerland. A more or less strong decrease in temperature must be suspected each year under our climatic conditions. This decrease in temperature can have a very negative influence on yield formation and particularly upon the number of pods and seeds per plant. Such cold-tolerant forms are known and will be collected and tested. At the present time such cold-tolerant varieties are also being investigated in Switzerland from the standpoint of yield formation and development. With cold tolerant varieties it should become possible to sow at an earlier date and by this way gain an additional temperature sum for the reproductive development.

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2) Study on the technique of crossing as well as on the genetic behavior of quantitative characters of soybeans.

During three years (1972 to 1974), studies were conducted on the technique of crossing as well as on the genetic behavior of quantitative characteristics of soybeans [Glycine max (L.) Merr.] by means of crossing varieties. In growth chambers, greenhouses and in the open field, 3,282 crosses were made. The rate of successful crosses was 17.9%, 14.5% and 6.2%, respectively, for the different years.

During the year 1972, different methods for the crossing were tested, with the following results:

9.2%	Castration with immediate pollination with fresh pollen
0.0%	Castration with immediate pollination with pollen from exsiccator
3.0%	Castration, pollination one day later with pollen from exsiccator
4.4%	Castration, pollination one day later with fresh pollen
2.0%	Castration, pollination one day later with pollen not stored in exsiccator

The method first mentioned was the most effective one. The storage of pollen in the exsiccator reduced its viability. The environmental conditions greatly influenced the rate of success of the crosses. In the open field this rate fluctuated during the day as well as from day to day. The most successful period was from 0700 to 1000 and 1700 to 1900. In order to obtain more knowledge of the best environmental conditions, crosses were made in growth chambers at different temperatures (17°C, 22°C, 27°C, 32°C during the day, 12°C, 17°C, 22°C, 27°C during the night). The best result (36.3% successful crosses) was obtained with the combination of 27°C/22°C. The success of crossing was also greatly influenced by the relative humidity (70-80% is necessary); the basis of the success, however, is a careful selection of the pollen.

During the three-year period the following crosses between varieties were made:

- 'Magna' x 'Merit', 0-52-903 x 'Dunn', Magna x 'Gieso' with the aim of increasing weight of 1000 seeds.
- 0-52-903 x 'Anoka' with the aim of improving earliness.
- 'Fiskeby' x Anoka and Fiskeby x Dunn with the aim of reaching maturity very early.

We investigated the following parameters: number of tillers, number of pods in the lowest 10 cm of the main stem, number of nodes, number of pods and seeds per plant, height of the plants, beginning of flowering, maturity, yield and weight of thousand seeds and also number of pods per node, number of seeds per pod, lodging and growth-type.

It was generally found that the values for these parameters fluctuated considerably depending upon the year and place but also depending upon variety and type of cross. The genetic behavior is subject to changes; generally we observed an intermediate type of inheritance. Our criterion for selection in these studies, i.e., the selection of plants with the best and the worst components of yield in the F_2, was not correct; the environment had too great an influence.

All of the parameters considered were closely related. Based on the correlation coefficients, we can state that differences in the yield were due mainly to a variable number of seeds per plant (67-94%) as well as the weight of thousand seeds (3-24%). The number of seeds per plant is correlated to the number of nodes per plant, the number of pods per node as well as the number of seeds per pod and the weight of thousand seeds; the main part of the variance is due to the number of nodes per plant.

The heritability is high considering parameters at the beginning of flowering and at maturity.

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1) Distant hybrids of soybean.

In the process of soybean selection a number of hybrids were obtained through crossing of wild (Glycine ussuriensis R. et Maack) and semicultured (Glycine gracilis Skvortz) soybean with a number of distinct and prospective varieties.

The results showed that cultured varieties have good crossing with wild and semicultured soybean and the ovary percentage of hybrid soybean is rather high (Table 1). The hybrids obtained have a number of advantages. They have a great number of small leaves with deep-green coloring, their stalks are not thick, and they are notable for their high disease resistance. Their vegetative mass contains a higher degree of protein and carotene.

Hybrids produced by means of wild and semicultured soybean give a large quantity of delicate vegetative mass that has a number of advantages and can be used both for silage and for dry vegetative mass production. The principal economic valuable features of hybrid lines being compared, as well as their origin, are given in Tables 2-5.

Experience showed that to eliminate some negative qualities of wild and semicultured soybean (such as small seeds, low resistance to lying flat, low grain number) it is necessary to conduct very complex crossings. Good results are received through crossing by means of one of the cultured parental varieties. Among numbers being compared, special attention should be paid to hybrids 286-4 and 287-242. They significantly exceed the yield of vegetative mass as compared with standard varieties; besides, they give high yield of seeds. Both vegetative mass and seeds of these hybrids have high content of protein and oil. It is necessary to note that carotene content in all hybrids received from crosses with wild and semicultured soybean is rather high. The only exception is hybrid 117-9.

Table 5 gives seed yield of a number of soybean hybrid lines. Among them is hybrid 175-27 which has exceeded average number of grain and seeds per plant 1.5 times as large. It has small seeds but it is not a drawback, because when being sowed as a fodder crop it will decrease a standard weight of seed per hectare. Almost all the hybrids listed in this table have the shortened vegetative season; most of them have higher content of oil in seeds though lower content of protein.

Thus the use of wild and semicultured soybean in selection can produce the valuable initial material which can give new varieties by means of further crossings.

'Nadia' variety was received through a.m. crossings and now it undergoes the investigation of the State Research Committee for Agricultural Crops. This variety was received through crossing of 'Peremoga' x ('VNIIMK 9186' x semicultured) and it has delicate high-quality vegetative mass and is recommended for dry vegetative mass production.

Table 1

The results of crossing of cultivated soybean with wild and semicultured varieties

	% of bean setting	
	Total	Including hybrids
Semicultured x [VNIIMK 9186 x Dnieprovskaya I(9)]	12	0
Kirovogradskaya 3 x Semicultured	4	100
Hybrid 342-10 x Semicultured	27	100
Ukrainskaya I x Creeping	40	100
Unlaid 2 x Creeping	12	20
Kirovogradskaya 3 x Wild	20	100
Ussuriyskaya 42 x Creeping	28	100
Kirovogradskaya I x Creeping	25	0
Semicultured x VNIIMK 9186	10	100
Lanka x Wild	33.3	100
Lanka x Semicultured	66.7	62.5
Kirovogradskaya 3 x Creeping	12.5	0
Wild x Semicultured	18.2	33.3
Rada x Semicultured	83.3	20.8
Wild x Semicultured (the second crossing)	13.3	50
Semicultured x Wild	20	50
Hybrid 342-10 x Semicultured	6.7	100

Table 2

The origin of hybrid numbers being compared (1976)

Hybrid number	Origin
117-9	Kirovogradskaya 3 x Wild
487-242	Peremoga x [(Illinny x Local Severokavkazskaya) x (VNIIMK 9186 x Wild)]
286-4	Peremoga x (VNIIMK 9186 x Semicultured)

Table 3

Indicators of productivity of silage numbers being compared (1976)

Number	Length of vegetative season (days)	Yield per hectare			Content			
					In seeds		In vegetative mass	
		Seeds	Vegetative mass	Hay	Protein (%)	Oil (%)	Protein (%)	Carotene (mg/kg)
Kirovogradskaya 3 standard	149	13.0	227	53.8	42.6	17.3	13.9	103.0
117-9	141	15.1	216	56.6	40.7	17.6	13.2	87.0
487-242	146	17.2	246	55.8	41.0	18.0	15.6	144.2
286-4	141	16.8	240	61.6	43.9	18.6	15.8	105.0

Table 4

Origin of hybrids being compared (1976)

Hybrid number	Origin
526-97/62	Kirovogradskaya 3 x [Peremoga x (VNIIMK 9186 x Semicultured)]
527-79/16	Kirovogradskaya 3 x [Peremoga x (VNIIMK 9186 x Semicultured)]
286-6	Peremoga x (VNIIMK 9186 x Semicultured)
175-27	Peremoga x (VNIIMK 9186 x Semicultured)
600-1-3	[(Kirovogradskaya 3 x Moishi-doe) x Korovogradskaya 3] x Semicultured
185-8/4	Peremoga x [(Illinny x local Severokavkazskaya) x (VNIIMK 9186 x Wild)]
185-186	Peremoga x [(Illinny x local Severokavkazskaya) x (VNIIMK 9186 x Wild)]
486-53	(Krasnodarskaya 13 x Yulka) x [Peremoga x (VNIIMK 9186 x Semicultured)]
532-218	VNIISK 1 x {Peremoga x [(Illinny x local Severokavkazskaya) x (VNIIMK 9186 x Wild)]}

Table 5

Characteristics of hybrids being compared obtained from crosses with wild or semicultured soybean according to economic value features (1976)

Hybrid number	Yield of seeds/ double center/ hectare	Height			Number per plant				Weight of seeds per plant	Weight of 1000 seeds (gr)	Content in seeds (%)		Length of vegetative season (days)
		Plant	Node	Pod	Branches	Node	Beans	Seeds			Protein	Oil	
Lanka standard	16.2	71.6	8.5	18.7	4.4	34.4	47.5	81.9	10.5	156.7	43.1	17.6	146
526-97/62	17.1	69.9	9.3	14.6	4.9	31.0	49.4	96.5	12.6	150.6	43.6	17.6	143
527-79/16	16.9	82.0	13.6	17.2	3.9	21.9	48.8	91.8	12.6	148.6	42.0	16.8	136
286-6	17.4	87.2	9.7	18.6	4.4	24.0	39.6	75.7	11.1	160.6	41.6	19.1	137
175-27	17.4	70.2	9.7	14.8	4.5	28.4	68.8	138.9	13.9	114.6	40.9	19.0	136
600-1-3	18.4	81.4	9.4	17.1	4.4	24.9	48.7	98.5	12.6	120.5	39.6	18.4	137
185-8/4	17.2	64.5	8.2	15.9	3.3	25.5	41.0	70.8	11.7	157.8	41.6	20.3	132
185-186	18.2	73.3	11.8	18.0	4.5	23.4	40.1	71.7	11.9	143.1	41.6	19.0	135
486-53	18.7	64.2	9.9	17.6	4.6	28.8	48.2	88.1	12.5	160.4	41.6	19.1	127
532-218	16.6	69.0	9.4	19.7	5.0	31.4	44.7	83.8	12.3	169.9	39.7	17.8	146

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1) Inheritance of time of flowering under short-day conditions.

Flowering in soybean is initiated by short daylength. There are several investigations exploring the genetic basis of the photoperiodic response in crop plants. However, such studies in soybean are quite limited. Bernard (1971) found that days to flowering in soybean is controlled by two genes, E_1 and E_2, which showed partial dominance for late flowering. A dominant gene, E_3, with a sensitive response to fluorescent light, was found to delay flowering and maturity compared to a reference cultivar, 'Blackhawk' (Buzzell, 1971). Thseng and Hosokawa (1972) reported two genes, AABB, that control the time of flowering. These genes had inter- and intra-allelic interaction.

The "decapitation technique" (Shanmugasundaram and Wang, 1977) was used on parents, F_1 and F_2 of four different crosses. One branch of each individual plant was subjected to 10-hr photoperiod while the other branch was subjected to 16-hr photoperiod. Days to flowering from planting was recorded for each branch.

The days to flowering of the parents, F_1 and F_2, under 10 hr and 16 hr are shown in Tables 1, 2, 3 and 4. Cultivar 'Shih Shih' and PI 194.647 are early while Acc. 2120, PI 230.970 and PI 230.971 are late under 10-hr photoperiod. Similarly the F_1 was early in all cases. Therefore, early flowering under the 10-hr photoperiod is dominant. In the F_2 of all four crosses studied, even though there is a range in days to flowering, the early individuals can be clearly cut at the 44 days to flowering. Above 45 days to flowering is late flowering. Therefore, under the 10-hr photoperiod the major gene effect on the time of flowering is fully manifested. The mode of segregation fits the expected 3 early : 1 late ratio very well (Tables 1, 2, 3 and 4). However, in the 16 hr the F_1 is partially dominant for late flowering and the time of flowering of the F_2 individuals shows a disturbed continuous distribution. It appears that under the 16-hr photoperiod the major gene action on the days to flowering is modified by either a few minor genes or an interaction of other genes involved.

Investigations on the relationship among E_1, E_2, A, B and the gene reported in this paper will be more meaningful for the tropical soybean breeding programs.

Table 1

Number of plants in the different days from planting to flowering class in parents, F_1 and F_2 of the cross Shih Shih x PI 230.970

Cultivar name or generation	Photo-period	Days to flowering class																	
		36	38	40	42	44	46	48	50	52	54	56	58	60	62	64	66	68	More than 70
Shih Shih	10-hr				4	6													
Shih Shih	16-hr					10													
PI 230.970	10-hr									10									
PI 230.970	16-hr																		10
F_1	10-hr			2	8	2													
F_1	16-hr														6	4	2		
F_2	10-hr	10	13	41	13	13	1	17	2	4	2								
F_2	16-hr	11	13	24	18	8		13	4	2	6	1	2	3	1				10

Source	Early	Late
F_2 segregation		
Observed	90	26
Expected (3:1 ratio)	87	29
χ^2 =	0.413	
P =	0.75 - 0.50	

Table 2

Number of plants in the different days from planting to flowering class in the parents, F_1 and F_2 of the cross Shih Shih x PI 230.971

Cultivar name or generation	Photo-period	Days to flowering class																		
		34	36	38	40	42	44	46	48	50	52	54	56	58	60	62	64	66	68	More than 70
Shih Shih	10-hr					4	6													
Shih Shih	16-hr						10													
PI 230.971	10-hr										10									
PI 230.971	16-hr																			10
F_1	10-hr				2	8														
F_1	16-hr																10			
F_2	10-hr	1	12	5	26	15	29		21	2	1	3	1	1	1	1	1	2		
F_2	16-hr	2	2	7	22	8	10		11	2	6	5	1	2						44

Source	Early	Late
F_2 segregation		
Observed	88.0	34.0
Expected (3:1 ratio)	91.5	30.5
χ^2 =	0.535	
P =	0.50 - 0.25	

Table 3

Number of plants in the different days from planting to flowering class in parents, F_1 and F_2 of the cross PI 194.647 x Acc. 2120 (Aug. 9, 1976 planting)

Cultivar name or generation	Photo-period	Days to flowering class																																
		30	32	34	36	38	40	42	44	46	48	50	52	54	56	58	60	62	64	66	68	70	72	74	76	78	80	82	84	86	88	90	92	>94
PI 194.647	10-hr	10																																
PI 194.647	16-hr	10																																
Acc. 2120	10-hr												6	6																				
Acc. 2120	16-hr																																	12
F_1	10-hr						5	2																										
F_1	16-hr																							7										
F_2	10-hr		8	12	38	12	21	13	20		16	5	19	2	2	1																		
F_2	16-hr	1	3	3	14	2	7	1	3		11		4	1	2	3	3	3		3	1	14	7	2	1	5	7	6		3	3		5	51

Source	Early	Late
F_2 segregation		
Observed	124.00	45.00
Expected (3:1 ratio)	126.75	42.25
χ^2 =	0.238	
P =	0.75 - 0.50	

Table 4

Number of plants in the different days from planting to flowering class in parents, F_1 and F_2 of the cross PI 194.647 x PI 230.970 (March 15, 1976 planting)

Cultivar name or generation	Photo-period	Days to flowering class																				
		30	32	34	36	38	40	42	44	46	48	50	52	54	56	58	60	62	64	66	68	> 70
PI 194.647	10-hr			5	5																	
PI 194.647	16-hr			10																		
PI 230.970	10-hr												10									
PI 230.970	16-hr																					10
F_1	10-hr							8	2													
F_1	16-hr																		2	8		
F_2	10-hr			12	20	4	19	29	18		7	4	5	3	2	2	1	1	1			
F_2	16-hr			11	17	3	20	3	7		7	7	4	7		1					4	37

Source	Early	Late
F_2 segregation		
Observed	102	26
Expected (3:1 ratio)	96	32
χ^2 =	1.5	
P =	0.25 - 0.1	

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2) Variation in the photoperiodic response to flowering in soybean.

Soybean cultivars representing each of the 10 U.S. Maturity Groups (MGS) (00 to VIII) were screened for the photoperiodic response to flowering from March, 1974 to June, 1974; another set was screened from October, 1974 to January, 1975 using natural daylength in the field as the short-day treatment. In another distant field artificial light was used to extend the natural daylength to 16 hr which represented the long-day treatment. In the March screening, 1,898 cultivars were screened while in October, 1,547 cultivars were screened.

The difference in days to flowering between the natural daylength treatment and the 16-hr treatment in general ranged from 0 to more than 90 days. In previous studies the photoperiodic response of soybean was classified as either sensitive or insensitive (Criswell and Hume, 1972; Polson, 1972; Asian Vegetable Research and Development Center, 1975; Nissly, 1976). Since different degrees of delay in the 16-hr photoperiod was observed, it was felt that to classify the cultivars according to the degree of delay in flowering might be practically useful. Therefore, a scoring method has been developed to classify the cultivars into different degrees of photoperiod sensitivity. The 10 different score classes are given on the following page.

Depending upon the need, sensitivity score 0 and 1 may be considered insensitive while scores 8 and 9 are the most sensitive. The frequency distribution of cultivars with each photoperiod sensitivity score for the two screenings are given in Tables 1 and 2. More low sensitive score (0 and 1) cultivars were observed in the early MGS. This agrees with the general statement that most of the cultivars insensitive to photoperiod belong

Table 1

Frequency of cultivars (%) in the different photoperiod sensitivity score (March 22, 1974 screening)

Maturity group	Photoperiod sensitivity score								Total no. of cultivars
	0	1	2	3	4	5	6	7 and above	
00	72.7	5.5	10.9	1.8	3.6	5.5	0.0	0.0	55
0	40.5	14.9	20.7	5.0	3.3	15.7	0.0	0.0	121
I	14.1	29.1	28.1	11.6	5.0	10.1	0.0	2.0	199
II	4.3	23.3	39.0	11.0	7.0	14.0	0.3	1.0	300
III	2.1	7.3	37.5	15.6	14.6	18.2	1.0	3.7	192
IV	1.0	2.0	21.0	19.7	14.2	26.8	3.1	12.2	295
V	0.0	0.0	9.2	11.8	14.5	32.9	3.9	27.6	76
VI	0.0	0.0	9.0	19.2	7.7	19.2	2.6	42.3	78
VII	0.0	0.0	0.0	0.0	3.6	0.9	0.9	94.6	112
VIII	0.0	0.0	2.9	0.0	0.0	0.0	0.0	97.1	35
Unknown	6.0	3.4	7.1	4.8	7.8	6.2	0.2	64.4	435
Pooled	8.6	9.7	20.2	10.3	8.5	14.0	1.0	27.6	1898

Table 2

Frequency of cultivars (%) in the different photoperiod sensitivity score (October 8, 1974 screening)

Maturity group	Photoperiod sensitivity score									Total no. of cultivars
	0	1	2	3	4	5	6	7	8 & 9	
00	84.9	12.3	2.7	0.0	0.0	0.0	0.0	0.0	0.0	73
0	50.4	29.1	12.1	4.3	2.6	1.7	0.0	0.0	0.0	117
I	36.3	30.2	21.4	7.7	2.2	1.6	0.5	0.0	0.0	182
II	31.8	31.8	20.6	7.7	5.2	1.0	0.7	0.3	0.7	286
III	22.7	25.4	24.9	11.6	12.7	0.0	1.7	1.1	0.0	181
IV	11.4	19.7	29.2	18.6	9.5	3.8	3.8	0.4	3.8	264
V	1.5	6.2	16.9	23.1	21.5	4.6	10.8	1.5	13.8	65
VI	8.6	11.4	32.9	11.4	14.3	10.0	1.4	2.9	7.1	70
VII	0.0	8.0	12.5	17.0	9.1	5.7	0.0	0.0	47.7	88
VIII	0.0	0.0	13.0	26.1	34.8	0.0	4.3	0.0	21.7	23
Unknown	13.6	10.6	12.6	13.6	11.1	4.5	1.5	0.0	32.3	198
Pooled	24.8	21.1	20.0	11.8	8.5	2.7	1.8	0.5	8.9	1547

Number of days delay under the 16-hr photoperiod	Sensitivity score
0 to 4	0
5 to 8	1
9 to 16	2
17 to 24	3
25 to 32	4
33 to 40	5
41 to 48	6
49 to 56	7
57 to 64	8
65 and above	9

to the early MGS (Criswell and Hume, 1972; Polson, 1972; Asian Vegetable Research and Development Center, 1975). However, no definite pattern between the MGS and the sensitivity score is observed. For the first time the photoperiod screening of cultivars from MGS IV to VIII are presented. Even though the number of cultivars with low sensitivity scores in the late MGS are very few when compared to the early MGS, cultivars with 1 and 2 sensitivity score were observed. Such photoperiod insensitive, late maturing cultivars may be better for breeding tropic-adapted soybeans than those in the earlier MGS. The early MG cultivars, when planted in the tropics, tend to flower too soon and therefore have low yields.

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1) A sterile mutant in progeny of a Forrest x Kent cross (Glycine max L.).

Sterile plants were found in an F_5 single-plant progeny row from a cross of 'Forrest' x 'Kent'. This sterility was observed in Row 15177 of the 1977 soybean breeding nursery grown at the Texas Agricultural Experiment Station, Lubbock, TX. Such sterility has not been previously reported in progeny of Forrest x Kent.

The single row segregated 35 fertile to 17 sterile plants. Sterile plants grew vigorously, developed small, seedless pods, and retained their leaves until frost. Although no cytological examinations of the sterile plants were made, the sterility closely resembles the st series reported by Hadley and Starnes (1964), Palmer (1974), and more recently by Winger, Palmer and Green (1977). The sterility is controlled by a single gene in the homozygous recessive condition. Two nonallelic asynaptic or desynaptic mutants, st_2 and st_3, were documented by Hadley and Starnes (1964), and st_4, a third nonallelic mutant, was reported by Palmer (1974). The fourth mutant reported by Winger, Palmer and Green (1977) was found to be allelic with st_2.

Seeds have been harvested from the 35 individual fertile plants, and a progeny test will be carried out to determine if segregation occurs. Until suitable tests for allelism can be completed, the mutant has been designated the "TAES Lubbock sterile".

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1) Field observation on rust reaction in M_3 soybean lines.

Soybean rust, caused by Phakopsora pachyrhizi Syd., is the most serious soybean disease in Thailand. The commonly grown varieties, S.J.1 and S.J.2, are susceptible to this disease. S.J.4, a new variety recently released by the Department of Agriculture, is only considered more tolerant than that of the mentioned varieties. There is a report on sources of resistant genes for this characteristic in existing germplasm collections (Bromfield and Yang, 1976). Some of them were tested in Thailand and were identified as either good to moderate tolerance (Pupipat, 1977) or susceptible (Nundhapun and Surin, 1977).

It is evident that a search for additional sources of rust-resistant genes is needed. At present, soybean mutation experiments for this purpose are being carried out at the Radiation and Isotopes Division, Kasetsart University.

The aim of this paper is to report a result on rust reaction observed in certain M_3 soybean lines grown in the field.

Twenty seeds each of 93 soybean lines (including 27 accessions from AVRDC) were irradiated with gamma rays of a caesium source at the dose of 15 krad. M_1 seeds, together with seeds of 3 susceptible lines as control, were grown in July, 1976 on Kasetsart campus. Eight hundred fifty-three M_1 plants of 92 lines were harvested. The M_2 seeds of each plant were sown as plant-to-row at Farm Suwan, Pakchong in January, 1977 (dry season). Unfortunately, 142 rows (from 14 lines) were damaged by the residual effects of atrazine in the soil. Only 711 M_3 sublines were harvested.

In the rainy season of 1977, 174 sublines (selected from a set of 3 sublines each having enough seeds for the test) derived from 58 lines were sown in replicated single-row plots 5 m long in the field at Farm Suwan, Pakchong (14.5°N).

About 64 days after planting the rust infections occurred in soybean plants. Another 14 days later the rust infections were very severe. Then, on October 14, 1977 the rust rating was carried out according to the International Working Group on Soybean Rust (IWGSR) rating system (Yang, 1977).

It was found that leaves on the upper third of the plant of three sublines which were derived from Line No. 123 (G8375, an AVRDC's accession), as well as one out of three sublines derived from Line No. 138 (Taichung), were

infected with non-sporulating lesions (332). The leaves on the upper third of the plant of other sublines including control lines were heavily covered with sporulating lesions (343).

It is still early to say that the four sublines producing lesions with no sporulation (hypersensitive reaction) which were found in this experiment are rust-resistant mutants. There is a need for further intensive investigation. Anyhow, this observation of the hypersensitive reaction type in M_3 soybean lines, especially the one out of three in Line No. 138 (Taichung) may suggest that an attempt to create variability for rust resistance by radiation should not be overlooked.

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1) A second gene for resistance to peanut mottle virus in soybean.

Soybean (Glycine max [L.] Merr.) was first reported as a natural host of peanut mottle virus (PMV) in 1972 by research workers in Georgia (Kuhn et al., 1972). PMV on soybean has since been reported in Virginia, South Carolina, Australia, and East Africa (Demski and Kuhn, 1977). Boerma and Kuhn (1976) reported resistance to PMV in soybeans to be conditioned by a completely dominant allele at a single locus. The objective of this study was to determine if there are other genes and/or alleles that might condition resistance to PMV.

During the winter of 1975-76, several soybean cultivars and Plant Introductions were tested in the greenhouse for reaction to PMV. Based on these tests, 20 resistant soybean cultivars and Plant Introductions and two susceptible lines were selected for intercrossing in 1976. Results reported here involve only five of the selected lines (Table 1). Each of the four resistant lines, 'Arksoy', 'Peking', PI 89.784 and PI 219.789, was crossed to a susceptible line, PI 229.315. Crosses were also made between Peking and each of the other three resistant lines (Table 2).

Table 1

Parents used in crosses in 1976

Identity	Maturity Group	PMV reaction
Arksoy	VI	Resistant
Peking	V	Resistant
PI 89.784[†]	III+	Resistant
PI 219.789	V	Resistant
PI 229.315	V	Susceptible

[†]Identity not certain since flower color does not agree with that reported in RSLM 238, April 1969.

The F_1 plants for each of the seven crosses were grown in the greenhouse during the winter of 1976-77. Flower, pubescence, hilum and seed coat colors were used as genetic markers to verify crosses in the F_1 and F_2 generations. The F_2 seedlings from individual F_1 plants were grown in metal flats in the greenhouse during summer and fall of 1977. Both F_1 and F_2 plants were inoculated with PMV and scored as either resistant or susceptible.

F_1 plants for each of the following crosses were resistant to PMV: Arksoy (R) x PI 229.315 (S); PI 89.784 (R) x PI 229.315 (S); and PI 229.315 (S) x PI 219.789 (R) (Table 2). Segregating F_2 progenies from the same three crosses gave an acceptable fit to a 3 R : 1 S genetic ratio. Thus it appears that resistance to PMV in Arksoy, PI 89.784, and PI 219.789 is controlled by a single dominant gene ($\underline{Rpv}_1$) as reported previously for soybean cultivars 'CNS' and 'Dorman' (Boerma and Kuhn, 1976). It is most probable that Arksoy and Dorman carry the same gene for resistance to PMV since Arksoy 2913 is a parent

Table 2

Reactions of F_1 and F_2 soybean plants to inoculation with peanut mottle virus (PMV) and probabilities of proposed genetic ratios

Cross	PMV reaction of F_1 plants	PMV reaction of F_2 plants			Proposed genetic ratio	Chi-square probability
		Res.	Susc.	Total		
Arksoy (R) x Peking (R)	R	86	17	103	13:3	.58
		49	14	63	13:3	.49
(Pooled data from two F_1 plants)		135	31	166	13:3	.98
Peking (R) x PI 89.784 (R)	R	36	8	44	13:3	.92
Peking (R) x PI 219.789 (R)	R	37	6	43	13:3	.44
Arksoy (R) x PI 229.315 (S)	R	45	10	55	3:1	.24
Peking (R) x PI 229.315 (S)	S	--*	--	--	---	---
PI 89.784 (R) x PI 229.315 (S)	R	37	13	50	3:1	.87
PI 229.315 (S) x PI 219.789 (R)	R	40	13	53	3:1	.94

*No F_2 data available at present.

of Dorman.

If the gene conditioning PMV resistance in Peking were the same as in the other three resistant lines, then one would not expect segregation in any F_2 families from crosses among these lines. However, segregation was observed in all F_2 families from crosses of Peking with the other resistant parents. Apparently, at least two different genes for resistance were present. The only two-class F_2 dihybrid ratio that would provide a reasonable fit to the data is 13 resistant : 3 susceptible. This ratio is possible if one assumes that Peking has a recessive gene for resistance. As shown in Table 2, the data provide a very acceptable fit to that model. The susceptible reaction of the F_1 plant from the cross Peking (R) x PI 229.315 (S) seems to further substantiate the hypothesis of a recessive gene for PMV resistance in Peking. The expected F_2 genetic ratio from that cross would be 1 R : 3 S. Data are not yet available.

Based on the available data, it appears that PMV resistance in Peking is conditioned by a gene in the recessive state which is independent of the single dominant gene reported by Boerma and Kuhn. While both PI 89.784 and PI 219.789 contain genes which interact with the Peking gene in a similar manner as that from Arksoy, it remains to be shown that they contain the same dominant allele. Investigations on the allelic relationships of sources of PMV resistance are being continued.

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1) Cytology of soybean haploid progeny.

Haploids are being isolated annually among individuals obtained from polyembryonic seeds associated with the North Carolina male sterile (ms_1).

The haploids are being used to obtain aneuploids. In 1976 and 1977, 7,206 and 15,530 seeds, respectively, were obtained from male sterile plants ($\underline{ms}_1$ North Carolina) representing Maturity Groups I-V. These seeds were germinated in the laboratory and screened for polyembryony in a search for soybean haploids (2n = 20). In 1976, five haploids were obtained from 167 polyembryonic seeds and one haploid was from a monoembryonic seed (Beversdorf and Bingham, 1977). In 1977, four haploids were obtained from 252 polyembryonic seeds. All monoembryonic progeny were screened phenotypically for haploidy; however, none was identified.

From the 1976 haploids, 45 seeds were obtained by either hand cross pollination with diploids or by about 10 apparent self pollinations. Most of these seeds germinated and progeny were grown in the greenhouse in 1977 and analyzed cytologically. The progeny consisted of 42 diploids, one triploid, one 70-chromosome plant, nine tetraploids, and only two trisomics. Ten seeds were obtained from the four 1977 haploids. These progeny consisted of nine diploids and one putative trisomic.

Currently, we are analyzing F_2 progeny from the trisomics for percent transmission. Palmer (1974) isolated several trisomics from asynaptic mutants and obtained a high percentage of trisomic progeny. Microsporocyte analysis of the F_1's was incomplete due to a lack of suitable diagnostic stages; however, restitution gametes in various stages of cytokinesis were frequently noted in most of the F_1's. Some spindle abnormalities including parallel spindles were also observed.

The predominantly euploid 2n = 40 progeny of haploid x diploid crosses suggest that the $\underline{ms}_1$ allele is functioning in these haploids to produce restitution gametes. This may occur in the male gametophyte by failure of cytokinesis as shown by Albertsen (1976), or in the female gametophyte by fusion of supernumerary nuclei found to be present at the time of fertilization (Cutter and Bingham, 1977).

A few trisomics are being obtained using haploids, but no monosomic or other deficiency aneuploids have yet been confirmed. The $\underline{ms}_1$ gene, which is carried by the haploids and which is associated with restitution gametes, is likely limiting the yield of both excess and deficiency aneuploids.

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2) Potential soybean vigor tests for screening at low germination temperatures.

Introduction: Littlejohns and Tanner (1976) have used soybean germination at low temperature (10°C) as a criterion for selecting for "cold tolerance". It is our contention that this coupled with a more definitive vigor test might prove to be more reliable in evaluating genotypic differences at low germination temperature. The most prominent soybean vigor tests have been classified into five major categories by McDonald (1976): (1) cold test, (2) accelerated aging test, (3) tetrazolium test, (4) respiration test, and (5) conductivity test. As McDonald has pointed out, most of these tests are somewhat subjective and have inherent problems associated with them. Our recent studies (Duke et al., 1977a; Duke et al., 1977b) have shown physiological and biochemical data which indicate that more quantitative methods may be used in testing soybean vigor, especially at low temperature (10°C). Our data relate to screening for cold tolerance and to all of the aforementioned vigor tests except the accelerated aging test, in that we have studied the effects of low temperature on soybean germination (cold test), mitochondrial respiration (respiration test), mitochondrial integrity (conductivity test), and dehydrogenases (tetrazolium test). In addition, we have studied the effects of low temperature on the production of asparagine, a major transport amino acid in soybeans, during germination. Presently it appears that three of the physiological and biochemical parameters mentioned here have potential as practical quantitative indicators of soybean vigor at low germination temperature.

Mitochondrial integrity: Glutamate dehydrogenase (GDH) may be used as an indicator of mitochondrial integrity because GDH is only located in mitochondria of etiolated plants (Duke and Ham, 1976). Our past studies have shown data similar to that in Table 1 which indicates that low temperature

Table 1

Percentages of GDH recovered in soybean (cv. Wells) mitochondrial pellets (20,000 g) germinated at optimal and suboptimal temperatures

		2 days	5 days	
Axes	10°C	39.7%	44.1%	Pellets were solubilized by freeze-thawing 3 to 5 times. GDH was assayed as previously described (Duke et al., 1975). Total GDH activities, from which percentages were calculated, were by the addition of supernatant (20,000 g) and mitochondrial (20,000 g) values.
	23°C	100.0%	100.0%	
Cotyledons	10°C	20.6%	26.8%	
	23°C	42.0%	38.2%	

has a great influence on mitochondrial integrity. When mitochondria are not fully developed, as in early stages of germination, their membranes are easily disturbed during extraction. Soluble enzymes, such as GDH, can then leak from mitochondria into mitochondrial extraction media. This may be what we are observing here: differences in stage of mitochondrial biogenesis. However, our previous study (Duke et al., 1977a) would suggest that membrane phase changes at low temperature could also account, in part, for differences in mitochondrial integrity.

From the data presented here it appears that axes values reflect the physiological states of mitochondria to a greater extent than cotyledon data. Presently we are conducting further tests to establish the validity of this test as an indicator of vigor in soybeans grown at low temperature.

NADP-isocitrate dehydrogenase (NADP-ICDH) activity: In a previous study (Duke et al., 1977a) we determined that increases in NADP-ICDH activity reflect the onset of germination of soybeans. This enzyme increased in activity before any of the other dehydrogenases assayed during germination. This would indicate that it might be very important in energy transduction early in germination. Also, we found that kinetic data from mitochondria were similar to those of NADP-ICDH at low temperature, indicating that this enzyme might be limiting at low temperature in soybean germination. We are currently investigating this assay as a possible screening device for soybeans at low temperature.

Free asparagine: Our previous study (Duke et al., 1977b) has shown that asparagine is higher in concentration than any other amino acid during soybean germination. Low temperature was shown to inhibit the production of asparagine from its precursor, aspartate. Table 2 indicates that differences in asparagine at 10° and 23°C are greatest in axes tissues. The asparagine assay is more complicated than either the NADP-ICDH assay or the test for mitochondrial integrity. However, it appears to be more indicative of vigor than the other tests. Presently we are attempting to find a more practical assay for asparagine.

Table 2

Concentrations* of aspartate and glutamate and their amide derivatives, asparagine and glutamine, in soybeans (cv. Wells) germinated at optimal and suboptimal temperature for 2 days

	23°C		10°C	
	Axes	Cotyledons	Axes	Cotyledons
asparagine	23.3	2.10	0	0.434
aspartate	1.34	3.21	2.98	0.706
glutamate	1.86	2.90	2.50	0.711
glutamine	0.55	1.15	0.964	0.064

*Concentrations are in μmoles g^{-1} fresh wt., and were determined by TLC.

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